

ABSTRACTS

INTERNATIONAL SCIENTIFIC
CONFERENCE

INFORMATION TECHNOLOGIES IN
THE RESEARCH OF BIODIVERSITY

(BIT - 2018)

SEPTEMBER 11-14, 2018
IRKUTSK, RUSSIA

ТЕЗИСЫ

МЕЖДУНАРОДНОЙ НАУЧНОЙ
КОНФЕРЕНЦИИ

ИНФОРМАЦИОННЫЕ ТЕХНОЛОГИИ В
ИССЛЕДОВАНИИ
БИОРАЗНООБРАЗИЯ

(BIT - 2018)

11-14 СЕНТЯБРЯ, 2018
ИРКУТСК, РОССИЯ

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ABSTRACTS OF THE CONFERENCE
“INFORMATION TECHNOLOGIES IN THE
RESEARCH OF BIODIVERSITY”
(BIT-2018)

IRKUTSK, RUSSIA, SEPTEMBER 11-14, 2018

IRKUTSK
ISDCT SB RAS

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Российского Фонда Фундаментальных Исследований
(РФФИ)

ТЕЗИСЫ ДОКЛАДОВ КОНФЕРЕНЦИИ
“ИНФОРМАЦИОННЫЕ ТЕХНОЛОГИИ В
ИССЛЕДОВАНИИ БИОРАЗНООБРАЗИЯ”
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Abstracts of the conference “Information Technologies in the Research of Biodiversity” (BIT - 2018). Irkutsk: ISDCT SB RAS, 2018. 120 p.

This volume contains proceedings of the Information Technologies in the Research of Biodiversity (BIT-2018). The conference tells about the latest developments in the field of integration of modern information technologies and classical research methods. New research requirements are being put forward, requiring the union of all researchers, standardization and unification of data and methods.

This volume is intended for researchers in the field of biology and computer science.

The conference was organized with the financial support of: Department of nanotechnology and information technologies of Russian Academy of Sciences; the Russian Foundation for Basic Research, Project no. 18-07-20053 Г.

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Тезисы докладов конференции “Информационные Технологии в Исследовании Биоразнообразия” (BIT - 2018). Иркутск : ИДСТУ СО РАН, 2018, 120 с.

Этот том содержит материалы конференции по Информационным Технологиям в Исследовании Биоразнообразия (BIT-2018). Конференция рассказывает о последних событиях в области интеграции современных информационных технологий и классических методов исследования биоразнообразия. Выдвигаются новые требования к проведению научных исследований, требующие координации всех исследователей, стандартизации и унификации данных и методов.

Этот том предназначен для исследователей в областях биологии и информатики.

Конференция проведена при финансовой поддержке: Отделения нанотехнологий и информационных технологий РАН (ОНИТ РАН); Российского Фонда Фундаментальных Исследований, Грант № 18-07-20053 Г.

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Preface

This volume contains abstracts of the International Scientific Conference “Information Technologies in the Research of Biodiversity” (BIT - 2018) that was organized in Irkutsk, Russia, during September 11-14, 2018.

The main purposes of the conference are.

- Coordination of research interactions to digitize, standardize and publish data on biodiversity in Russia and other countries, as well as promoting and spreading modern international principles, resources and tools for working with biological data.
- Consideration of modern principles for creating and integrating local and regional information system projects for biodiversity research in Russia and other countries.
- Creation of infrastructures for implementing technological and information support to organizations seeking to exchange data and data analysis methods.
- Development of specialized software for handling biodiversity research tasks.
- Networking and exchange of experience, advanced technologies and trends in the field of distributed databases and data processing.

The main topics of the conference are.

- Global biodiversity data portals: data integration, use in knowledge generation tasks.
- Information and analytical systems on biodiversity. Virtual natural history collections.
- National data on biodiversity: the current state of digitization. Copyright issues, methods and concepts for assessing data quality.
- Theoretical fundamentals and organization technologies of the information and telecommunications infrastructures. Standards for describing digital data, processing services, etc.
- Methods, models, software systems and Web services for the analysis of biodiversity data.
- Application of remote methods in vegetation mapping and biodiversity research.

Предисловие

Этот том содержит тезисы докладов конференции по Информационным Технологиям в Исследовании Биоразнообразия (BIT - 2018), место и дата проведения: Иркутск, Россия, 11–14 Сентября, 2018.

Цели конференции.

- Координация взаимодействий по оцифровке, стандартизации и публикации данных по биоразнообразию в России и других странах. Популяризация и распространение современных международных стандартов, ресурсов и инструментов для работы с биологическими данными.
- Рассмотрение современных принципов создания и объединения локальных и региональных проектов информационных систем исследования биоразнообразия в России и других странах.
- Создание инфраструктур, реализующих технологическую и информационную поддержку организации обмена данными и методами анализа данных.
- Развитие специализированного программного обеспечения для решения задач по исследованию биоразнообразия.
- Обмен опытом, передовыми технологиями и тенденциями в области распределенных баз данных и распределенной обработки данных.

Тематика конференции.

- Глобальные порталы данных о биоразнообразии: интеграция данных, использование в задачах генерации знаний.
- Информационно-аналитические системы по биоразнообразию. Электронные биологические коллекции.
- Национальные данные о биоразнообразии: современное состояние оцифровки. Вопросы авторских прав, методы и концепции оценки качества данных.
- Теоретические основы и технологии организации информационно-телекоммуникационных инфраструктур. Стандарты описания цифровых данных, сервисов обработки и т.д.
- Методы, модели, программные системы и Веб-сервисы для анализа данных о биоразнообразии.
- Применение дистанционных методов в картографировании растительности и изучении биоразнообразия.

Organization

BIT-2018 is organized by Matrosov Institute for System Dynamics and Control Theory of Siberian Branch of Russian Academy of Sciences in co-operation with Siberian Institute of Plant Physiology and Biochemistry of Siberian Branch of Russian Academy of Sciences, V.B. Sochava Institute of Geography of Siberian Branch of Russian Academy of Sciences, and Institute of Mathematical Problems of Biology RAS – the Branch of the Keldysh Institute of Applied Mathematics of the Russian Academy of Sciences. With the support of GBIF: the Global Biodiversity Information Facility and Department of nanotechnology and information technologies of Russian Academy of Sciences.

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Actualization of herbarium labels information

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Актуализация информации гербарных этикеток

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Data on Russia's bryoflora have a centralized accumulation platform - the database (DB) of the Moss Flora of Russia (<http://arctoa.ru/Flora/basa.php>). The DB intensively develops; now it reached more than 130 000 records; the volume achieved mainly by combining of personal DB of currently working Russian bryologists. In recent decades organization of own working materials in the form of desktop DB has become a common practice in botanical investigations. However, the information of huge herbarium collections remains inaccessible for operative and especially remote work. Mass scanning of herbarium specimens without label decoding does not solve the problem. In the case of bryophytes scanning of herbarium labels without label decoding turns into "information noise": Internet search engines by the query for moss species name gives not photos or drawings of the species, but hundreds of label scans, that in unsystematized form have no scientific sense. Mass scanning of herbarium specimens has to go along with mass entering into a DB of herbarium labels, however it is an extremely laborious task (and in the case of large herbariums and small or absent assistant staff it looks to be impossible task). So, in the Moss Flora of Russia DB (MFR-DB) there are absolutely not presented voluminous bryological herbaria collected by the deceased scientists V.L. Bardunov (IRK), V.Ya. Cherdantseva (VLA), P.N. Krylov and E. Ya. Muldiyarov (TC), A.N. Vasiliev (KRAS). The lack of information distorts the general picture of moss species distribution. For this reason some regions (Irkutsk and Tomsk Provinces, Tyva, Khakassia, the

south of the Krasnoyarsk Territory) are "white spots" on the maps generated by the MFR-DB. To speed up of herbarium labels data transformation into electronic form a DB in MS Access was made. The interface of the DB uses fields with drop-down lists to enter the main part of text data. An important and convenient feature of the software is implementation of procedure for updating lists of locations, habitats and collectors. They are replenished in parallel with filling of the DB and updated every time you enter a new record. As a result, instead of the routine input of labels data (very often repeating), the user only needs to select the desired value in the drop-down list or enters the initial letters of the text in the field and the desired value will be selected automatically. Lists include non-repeating field values that occur in the labels of samples collected on the same day, that makes them compact and easy to use. Initially, the software was created by I.Artemov as Vascular Flora BD of the Tuva division of Herbarium of The Central Siberian botanical garden (NS) . Its convenience prompted the remaining authors to take up inventory of the old non-arranged bryological collections NSK and IRK, that is in process now.

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Analysis of anthropogenic pressures on the ecosystem of lake Baikal method of mathematical statistics

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Currently one of the most important challenges humanity becomes a natural water pollution substances of anthropogenic nature. With the vast array of data obtained during the monitoring observations, using statistical methods allows you to identify the major patterns and complex approach to the solution of the problem. Studied microorganisms isolated from a variety of ecological niches of the ecosystem of the Lake Baikal on

presence of the enzymes of the ER. Found that microorganisms are indicators of anthropogenic influence on the early stage of water pollution. The analysis for the presence of enzymes of restriction endonucleases (ER) was carried out. Long-term studies have established that a large variety of ERs is found in bacterial strains isolated from samples sampled in places where anthropogenic influence is observed (Listvyanka, Baikal). It was revealed that under the influence of human activity there are significant disturbances in the biosynthesis of ER enzymes in bacteria. Restriction enzymes, previously known only theoretically, were found in areas of anthropogenic influence. In the strains of bacteria isolated from the clean sections of the lake, all the ERs that we discovered are well known. To identify the conditions for the synthesis of restriction enzymes (ER) in the coastal part of the lake ecosystem. Baikal in a certain place of sampling during cluster analysis, 28 types of different types of ER were identified. Frequency of occurrence of enzymes ER can be divided into several types: 1) rare restriction enzymes (found only in a strain of a bacterium isolated from only one sample) include AccI, NcoI, Sall, ScaII, HpaII, Fnu4HI, HgiEII, NruI, HgiCI, AvaII, MwoI, CeuI; 2) a relatively small spread of ER (found in 2-4 samples), including XhoI, BpuII, EcoRV, BclI, XhoII, EspI, DraII, EcoRII, SmaI, BamHI; 3) fairly common ER (identified in 6-13 samples), these include HaeIII, ClaI, MboI, PstI. It should be noted that the most common restriction enzyme MboI was found 14 samples, and this leaves 21% of the total number of investigated (66 samples), all other ERs were less common (1.5% - 15% of all analyzed samples). When analyzing the data obtained, it was revealed that the sampling areas differ greatly in the number of detectable ERs (from 1 to 7). The larger the binary distance, the more differences in the spectrum of detectable ER. Differences in binary distance reach 1 (100%), which means that ERs occurring at one point of selection are not found in samples taken elsewhere. There are two pairs of sampling points, where their spectra do not differ. Within each pair of these points, the ERs were of the same type, but the pairs themselves were different (binary distance 1 -100%). Among the methods of statistical analysis (calculation of medians, graphic visualization of indicators, cluster analysis) the most informational method turned out to be a cluster analysis using UPGMA method with calculation of distances on the Euclidean distance measure. As the result of the research, has set many hidden factors described. Asked when the vast array of received data to identify causal relationships between variables, variability and use dispersion and correlation analysis methods. Use methods of statistical

analysis allows you to identify the major patterns and complex approach to the solution of the problem. Thus, in the vast array of data obtained as the result of the research methods of statistical analysis to identify cause-and-effect relationships, determine the strength and direction of variability between variables and are considered one of the promising.

Analysis of diatoms using the logical method search

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Анализ диатомовых водорослей с использованием логического метода поиска

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One of the methods of monitoring of the Baikal Lake ecosystem is the analysis of diatoms. Such analysis is performed in LIN SB RAS. Diatoms are very demanding to conditions of the environment, so sometimes their number in specific periods is considered to be one of the indicators of the ecological condition of the Baikal Lake. Nowadays the task of calculation of diatoms numbers is performed manually by microscope operator which is very time-consuming process. In order to solve such kind of tasks certain software tools have been developed, which allow to measure length and width of objects, scale and view images. These tools have various filters that improve image perception. However, application of their tools to solution of this problem is not possible due to certain limitations: some of software tools support only specific microscope models, some tools do not perform diatom extraction. All of the software tools are not able to automatically distinguish diatoms according to their types. The complexity of this task is caused by differences in diatoms shape (square, round, linear etc.), size and texture. The method based on logic programming for image understanding is proposed in order to solve the diatom extraction problem. This method is suitable for diatoms extraction, as it allows

describing every type of diatoms and performing the search. The diatom type description is a rule in Spatial Object Query Language (SOQL). The diatom shape is described using the relation of the graphical primitives, such as line, circle or their combinations. More complex shapes, for example, polygons, can be described using their combinations. Length and width can be defined with the size of graphical primitives, the texture can be defined with pre-defined model. The example of the rule for extraction of diatoms with rectangle shape: $\text{diatom}(A,B,C,D) :- \text{line}(A,B), \text{line}(B,C), \text{line}(C,D), \text{line}(D,A), \text{dist}(A,B) > 25, \text{dist}(A,B) < 40, \text{dist}(B,C) = 60, \text{dist}(B,C) = \text{dist}(A,D), \text{angle}(A,B,C) = 90, \text{angle}(B,C,D) = 90, \text{angle}(C,D,A) = 90, \text{texture}(A,B,C,D, \text{diatom_texture}).$

The algorithm has following steps:

1. User sets the threshold value of Energy function.
2. Features are being extracted from the image in the process of logical conclusion. It uses Deep First Search method (DFS).
3. Once the desired feature combination which satisfies the rule is found, the value of Energy function is computed and compared with the threshold. If the value is less than threshold then diatoms are extracted, otherwise the search will continue.
4. Repeat step 3 until all possible combinations are not found. One of the advantages of the proposed method is that it allows creating description of various, even not discovered yet, diatom types in short period of time and perform their search. The method is robust to noise, blur and other collisions, however usually method takes a lot of time to complete.

Analysis of the competitive relationship and the possibility of a sympatric habitat of native *Castor fiber* and alien *Castor Canadensis* on the territory of the European part of Russia

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Анализ конкурентного отношения и возможности симпатрического обитания нативного *Castor fiber* и чужеродного *Castor Canadensis* на территории Европейской части России

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The appearance of Canadian beaver *C. Canadensis* (Cc) in Finland in 1937 was associated with the intentional introduction of seven individuals of that species with the purpose of restoring the almost extinct Eurasian beaver *C. fiber* (Cf). In those years, many zoologists recognized only one species. However, in 1973, karyological studies showed the species differences between New World (Cc : chromosomal number (cn) =40) and Old World (Cf : cn=48) beavers, therefore Cc became an alien species in Eurasia. In the 50s of the XXth century, after the introduction of Cc into the territory of Finland (1937), Canadian beavers had penetrated into the territory of Russia and continued to expand their range. It is assumed that there is a process of interpenetration and replacement of one species of beavers by another in the Karelian Isthmus of Leningrad Region, as well as in Arkhangelsk Region. Analysis of the literature data shows that there is no an entire opinion on the competitive relationship of two species in the future. The aim of the work is to analyze the competitive relations between two beaver species, Cf and Cc, and give the forecast of the dynamics of the abundance of these species in the European part of Russian territory. To achieve this goal, the following tasks were accomplished: 1. Modern trends in the development of two beaver species populations in the territory of model Natural reserves and the subjects of the European part of Russia were characterized; 2. The potential capacity of beaver habitats in the European part of Russia was estimated; 3. The integral estimation of biological similarity / difference of two beaver species in the same habitat conditions was given and an integrated raster-vector database including results of beaver settlements research was created. In general, the parameters determining the similarities and differences in many aspects of the biology of two species, Cf and Cc - fertility, family size, rate of

maturity, life span and age composition of populations of both species - were revealed. Such parameters explained the competitive advantage of Cc and possible replacement of aboriginal Cf by foreign Cc . The two-species model analysis used has shown the validity of the G.F Gause principle of competitive exclusion, i.e. the population of Cc in the joint use of spatial and fodder resources grows faster and limits the population of Cf, so if the external conditions remain unchanged, the Cf population may die out in time. Numerical experiment has shown that for different ecological conditions of Laplandsky, Darvinsky, Prioksko-Terrasny, Central-Forest Oksky and Khopersky reserves, the commencement of replacement varies from 50 to 245 years. Data analysis using a two-species model was implemented with the financial support of the RSF grant No. 16-14-10323 and data collection by the programs of the Presidium of the Russian Academy of Sciences № 41 “Biodiversity of natural systems and biological resources of Russia”.

ANIS: “Accuracy of ecological Niches Improved by Satellite”

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ANIS: “Accuracy of ecological Niches Improved by Satellite”. In recent years, ecological niches models (ENM) and species distributions models (SDMs) have developed tremendously for conservation purposes and for estimating the impacts of global change. The main objective of ANIS project is to take full advantage of the new generation of remote sensing data to refine SDM predictions by improving the quantification of suitable habitats for species in ENM, in complement to classically used factors. The idea is also to make the best of the recent developments in deep learning technologies which are able to integrate highly nonlinear and heterogeneous data, to take advantage of the availability of large volumes of species occurrence data on GBIF (Global Biodiversity Information Facility) in order

to initiate a new generation of ENMs. Deep learning techniques, particularly adapted to process highly heterogeneous data in large volumes, will be used as follows: For each species, a set of occurrences will be selected on GBIF and other portals, and available data related to the occurrence locations will be used to train and test the deep neural networks (DNN). For each occurrence, the following data will be used when available: remotely-sensed information from satellite images around the occurrence location, temperature, rainfall, hygrometry, altitude, type of soil if known, georeferenced field landscape pictures around the location, other species living nearby, so as to take interactions between species into account. The models and distributions of species at global, regional and local scales resulting from the project will be made available to the scientific community and stakeholders through a dedicated portal.

Application of remote sensing methods for landscape mapping of the Mondy depression

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Применение дистанционных методов для ландшафтного картографирования Мондинской котловины

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A method of typological mapping of landscapes with the use of Landsat satellite images and the digital elevation model SRTM, as well as the method of factorial-dynamic classification of landscapes, was developed and a large-scale landscape map of the Mondy basin was created. At the first stage, the image was automatically classified using the neural network classification method, resulting in a picture divided into 11 classes. The resulting classified image was smoothed to remove the mosaic effect and translated into a vector map. For each unit obtained as a result of the

classification of the satellite image, the following parameters were calculated by means of spatial analysis in the GIS: belonging to a particular ridge, category according to the classification of the image, height category, slopes and topographic wetness index. By the combination of these parameters, each unit was assigned to a certain type of landscapes. In the study area on the Tunkinsky goltsy ridge goltsy steep slope screes with lichen cover landscapes, as well as birch and larch-birch stages of restoration of larch forests are dominated, and on the Khamar-Daban ridge – larch moss and dwarf birch forests, as well as meadows with the community of dwarf birch. The work was carried out within the framework of the program of the V. B. Sochava Institute of Geography SB RAS with partial support of the Russian Foundation for Basic Research (projects No. 17-05-00588 and No. 16-05-00902).

Assessment of typological diversity of vegetation cover on the basis of field data, RSD and DEM on the example of the western part of the Moscow Region.

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Оценка типологического биоразнообразия растительного покрова на основе полевых данных, ДДЗ и ЦМР на примере западной части Московской области.

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Assessment of biodiversity and its determinants is an urgent task of modern science. To assess the ecosystem (typological) biodiversity of vegetation at the regional level, the main source of data is field research. Such data are point and do not give an idea of the spatial variation of types of plant communities. Data on the relief and / or reflective characteristics of vegetation obtained from satellites in different spectral ranges can serve as sources of quasi-continuous information for the interpolation of typological vegetation units. The relief (DEM) is the basis for the redistribution of material-energy flows of various levels. Multispectral remote sensing data (RSD) fix the reflection/absorption of solar radiation by vegetation, which allows obtaining information about its state and functioning. There are several methods for interpolating data based on the training sample, but most of them require significant computational resources for large sample sizes. Stepwise discriminant analysis, under certain restrictions, allows processing large data sets and explicitly separates classes, which is important in interpreting biodiversity factors. As an example of such an analysis is considered the territory of the western part of the Moscow region, which has a complex structure of vegetation cover due to both natural and anthropogenic factors. Based on 1087 geobotanical descriptions, 38 syntaxes in the rank of associative groups and 5 categories of vegetation types not included in the classification (small grass mixed grass, grassy meadow cuttings, meadows, open waterlogged habitats and shrubby wet grass) were identified using the eco-phytocenotic approach . In addition, 3 categories of vegetation cover (fields, reservoirs and settlements) were identified on the basis of RSD. The overall quality of discrimination of the allocated units from the projective covering of species in accordance with the descriptions of vegetation was 84.5%. The source of information about the relief of the territory was SRTM data, for which the relief characteristics (gradients, curvatures, illumination) of various levels of the hierarchical organization were calculated. The quality of discrimination of plant units on the basis of DEM was 49.6%. Landsat 5 and 8, combined in mosaics for March, August and September and spectral indices calculated on the basis of research channels were used as RSD. The quality of discriminant analysis in this case was 49.8%. The quality of discrimination conducted in the joint analysis of DEM and RSD was 64.6%. Thus, the joint use of information on the relief and RSD improves the allocation of allocated classes by 15%. A cartographic model of the typological diversity of vegetation cover was developed.

Biodiversity data mobilization in the Prioksko-Terrasnyi Biosphere Reserve

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Мобилизация данных о биоразнообразии Приокско-Террасного биосферного резервата

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The Prioksko-Terrasnyi Biosphere Reserve (PTZ) was founded in 1945 and has been a part of UNESCO World Wide Network of Biosphere Reserves since 1978. Biodiversity data mobilisation via global portals is important activity of the Reserve. PTZ became a GBIF publisher in 2016 and was the first Russian Biosphere Reserve in GBIF network. Data mobilization is carried out through IPT Installation of the Institute of Mathematical Problems of Biology (Russian GBIF IPT). About 27000 occurrences have been published by PTZ through GBIF.org (3 occurrence and 2 checklist datasets). The largest dataset contains the results of phenological observations on the PTZ from 1948 to 2016 (24358 occurrences, doi 10.15468/2txjmp). This data is used in the international projet Chronicle of Nature: Large Scale Analysis of Changing Eurasia Ecosystems (ECN). The spiders ((Arachnida: Aranei)) are studied in detail among another taxonomic groups. Total of 284 spider species belonging to 145 genera were founded in the Reserve, checklist of this group available via GBIF (doi 10.15468/819bz7). The results of two-year field studies of spiders in nine different habitats of PTZ are presented in a separate occurrence dataset (doi 10.15468/3cbyt7). Biological collections of PTZ are not digitized. However, generalized data of labels for herbarium collection already available through GBIF (doi 10.15468/r8ybnq). We will plan to expand this data by images of specimens. Published datasets are cited in 3 English-language articles in less than 2 years since the publication of the

first dataset. Some biodiversity data for PTZ also available via iNaturalist system (www.inaturalist.org). It is a citizen science project and online social network of naturalists, citizen scientists, and biologists. The iNaturalist platform is very important for promotion of ecological education in the Reserve.

Biodiversity of Cenozoic ochotonids (Ochotonidae, Lagomorpha, Mammalia) in Holarctic

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Биоразнообразие пищух ((Ochotonidae, Lagomorpha, Mammalia) Голарктики

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Ochotonids are originated in the Central Asia at the early Late Oligocene when Eocene climate changed towards dry and continental that led to initial aridification. Tropical forest declined gradually and open landscapes, favourable ochotonids habitat, began to distribute. The family Ochotonidae consists of two subfamilies – Sinolagomyinae and Ochotoninae. The earliest ochotonids - sinolagomyins - were represented by the genera Bohlinotona and Sinolagomys, of which the first appeared to be the most archaic form displaying some feature with leporids by having reduced M3. Bohlinotona pusilla, known from Saint Jacques, China and the locality Shine Us, Mongolia, from the earliest stage of the Late Oligocene, is characterized by well developed roots. Advanced form Bohlinotona sp. known from a number of sites in Mongolia of the second part of Late Oligocene lack of roots completely and they differ much from B. pusilla morphologically. To the end of Oligocene Bohlinotona disappeared. The genus Sinolagomys includes at least 7 species widely distributed in China, Mongolia and Kazakhstan and to the end of Early Miocene they disappeared. Significant reorganisations in paleoenvironment of Eurasia occurred in Oligocene-Miocene transition time. Landbridge between Asia

and Africa and Asia and North America appeared to serve as a migration road to exchange of fauna. Two ochotonid genera – *Austrolagomys* and *Kenyalagomys* are known in Miocene fauna of Africa. At that time ochotonids migrated to North America, that evidenced by the genus *Oreolagus* having diverse species. With the climate becoming more continental and arid at the beginning of Miocene open landscapes became widespread in Eurasia. Ochotonids distinguished to Europe, they were represented by genera *Heterolagus*, *Lagopsis*, *Marcuinomys*, *Albertona*, *Paludotona* having diverse taxa. In Asia ochotonids were abundant and contain a number of diverse taxa. The characteristic Asian genera are *Bellatona*, *Bellatonoides*, *Alloptox*, *Ochotonoma*, *Ochotonoides*, *Proochotona* a.o. The Pliocene time with mild and warm climate became the favourable time for ochotonid diversification, especially for the genera *Pliolagomys*, *Ochotonoides* and *Ochotona*, known in the Europe, North America and Asia, they were represented by more than 50 extinct species. At the end of Pliocene all ochotonid genera disappeared except of the genus *Ochotona*, which continued to exist at the present time. Approximately 30 extant species are known of the world, one species in the Europe, two in North America and 28 taxa are known in Asian fauna.

Biodiversity of late Cenozoic small mammals of the south Eastern Siberia

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Биоразнообразие мелких млекопитающих позднего кайнозоя юга Восточной Сибири

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The studied area, south of East Siberia, consists of two territories – Transbaikalia and Prebaikalia. The small mammal (lagomorphs and rodents) record of the region covers the time span from the Late Oligocene

to the Recent time. They are the important components of modern and past mammalian faunas of Siberia. They belong at least to 12 families including more than 40 genera. The earliest fossil records are scarce, they include Late Oligocene taxa. Miocene faunas are much more diverse known from sites Aya, Tagai and Saray. The characteristic taxa belong to lagomorphs and rodents. The diversity of early Pliocene faunas is high, they are represented by the genera *Hypolagus*, *Stachomys*, *Lophocricetus*, *Sicista*, *Ochotonoides*, *Prosiphneus*, *Microtodon*, *Microtoscopes*, *Promimomys* including numerous species. At the Late Pliocene the fauna is characterized by disappearance of a number of archaic arvicolids and by increasing abundance and diversity of small mammals containing diverse lagomorphs (*Hypolagus*, *Ochotonoides*, *Ochotona*) and murids (*Orientalomys*, *Micromys*). For the first time arvicolids genera appeared, they are *Mimomys*, *Villanyia*, *Pitymimomys*. Moreover hamsters of the genera *Kowalskia*, *Cricetinus*, *Cricetulus* and a peculiar genus *Gromovia* are known also. The characteristic feature of the Early Pleistocene small mammalian faunas is an explosive radiation and abundance of ground squirrel *Spermophilus* and the first appearance of the genera *Clethrionomys*, *Cromeromys*, *Allactaga*, the reduction in number and quantity of rooted voles *Mimomys* and *Villanyia*. *Zokor* *Mesosiphneus* was replaced by more advanced species. The significant reorganizations in small mammal assemblages at that time occurred due to the climatic changes towards cooler and drier. Gradually Pliocene taxa vanished and new genera of voles appeared. At the Middle Pleistocene with further strengthening of arid conditions the inhabitants of dry landscapes became dominant forms in the fauna. During the Late Pleistocene periglacial conditions were established in the region and cold open landscapes were distributed widely.

Building a national biodiversity information facility in Norway

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Norway joined GBIF in 2004 as the 31st national country to sign the memorandum of understanding as voting participant. The Norwegian

membership in GBIF was ratified by the Ministry of Education and Research. The role as Head of Delegation (HoD) with voting rights in the GBIF Governing Board was from the start delegated to the Research Council of Norway (RCN). The role as Head of Delegation was in 2017 delegated to the Natural History Museum of the University of Oslo. The GBIF Participant Node for Norway was established 1st of June 2005 at the Natural History Museum of the University of Oslo (UiO-NHM) where the Node has been operative until today through a series of in total four funding periods (2005 to 2007, 2008 to 2011, 2012 to 2016, and 2017-2019). The Norwegian GBIF-node has (more or less) two dedicated full-time staff members and operates in close collaboration and sharing of responsibilities with the Norwegian Biodiversity Information Centre (NBIC) in Trondheim. Together with the ForBio Research School in Biosystematics (ForBio), the Norwegian GBIF-node will collaborate on open data publication training in Russia and former Soviet countries in the Central Asia and Caucasus region during the next years with funding from the Norwegian Centre for International Cooperation in Education (SIU). Following the international conference on “Information Technologies in the Research of Biodiversity” in Irkutsk (11 to 14 September 2018), a training course on open data mobilization using GBIF and BOLD tools (15 to 19 September 2018) will be organized by ForBio in collaboration with GBIF, the University of Bergen and the Norwegian University of Science and Technology, as part of the SIU funded MEDUSA project. A similar workshop with funding from SIU was organized by ForBio and GBIF together with the Shirshov Institute of Oceanology in Moscow from 15 to 17 May 2018 on “Digitization of collections and publishing data from wet collections”. The BioDATA project by ForBio and GBIF with funding from SIU will organize a three-year training program (during 2018 to 2021) on open data mobilization together with partners from Armenia, Belarus, Tajikistan, Belarus and Ukraine.

CAMPUS-S – the model of ground layer vegetation in forest ecosystems and their contribution to the dynamics of carbon and nitrogen

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CAMPUS-S – модель популяций растений живого напочвенного покрова лесных экосистем и их вклада в динамику углерода и азота

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The role of ground layer vegetation is rarely taken into account when analyzing the carbon balance of the forest ecosystems. A contribution of ground layer vegetation plants to carbon cycle in forest ecosystems can also be significant. Ground layer vegetation is one of the leading factors influencing the process of renewal, germination of seeds, and further development of seedlings both under the canopy of the stand and on felling areas. There are 4 types of impacts that the ground layer vegetation has on forest regeneration processes: mechanical (a dense lichen cover can prevent the penetration of seeds into the soil); physical (the creation of a microclimate); physiological (plants of ground layer vegetation create competition for elements of nutrition, moisture); biochemical (influence mediated by the release of herbs of phytoncides and colins by some species). These effects can be combined in different ways and, as a result, have both a positive and negative effect on the first stages of forest renewal. Due to the lack of tools to predict the structural and functional dynamics of populations of herbaceous and shrubby plants, we developed the model CAMPUS-S. The developed model CAMPUS-S uses several modeling techniques: matrix modeling, L-systems technology and cellular automata modeling. Species-specific data due to the genotype are defined as input data (using the technique of L-systems) for each ontogenetic state, but their implementation in the course of modeling depends on external conditions (the technique of cellular automata is applied). To implement the polyvariance of the transitions between ontogenetic states, the matrix modeling method is used. The CAMPUS-S model consists of two main submodels: a submodel of the structure of populations of the ground layer vegetation and a submodel for calculating the dynamics of biophilic elements (carbon and nitrogen) in plants of the ground layer vegetation and soil. The space in the CAMPUS-S model is heterogeneous. The input module allows generating or dynamic loading of the map of the microrelief, according to which

the temperature and moisture of the organic and mineral horizons of the soil are distributed in space during the simulation, and a map of locations that are inaccessible to the simulated plants (imitation of large stones, tree trunks). The irradiance map under the canopy is dynamically transferred from the EFIMOD model. The climatic data necessary for the functioning of the model (temperature and moisture of the organic and mineral horizon of the soil) are generated by the statistical simulator of soil climate (SCLISS). For climate parameters, a standard deviation is specified, which allows to regulate the oscillations of these parameters at different points of the simulated territory. To implement the feedback mechanism between plants and soil, the integration with the ROMUL-HUM model was implemented. The work was supported by the RFBR (18-34-00556) and the RSF (18-14-00362).

Climate data optimization for species distribution models using unsupervised machine learning

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Оптимизация климатических данных для моделирования распространения видов с помощью машинного обучения без учителя.

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Species distribution models (SDMs) attract growing interest of ecologists and related domain experts as a tool to connect observations of species occurrence and environmental factors as well as to predict taxon's geographical distribution. Model realism and robustness are influenced by predictor relevancy, modelling method used, and various settings. Currently entropy maximization approach implemented in MaxEnt Software gained the most attention, its alternative implementations are also available. At the same time, the plethora of different machine learning techniques might also be

helpful for SDMs optimization. To address the problem we used 19 bioclimatic variables taken from Worldclim database (version 2.0) with for Crimean peninsula the resolution of 15" as predictors. Actual localities of Apiacea representatives were obtained from 3 russian herbarium (MW, MHA, LE) specimen tags. For 3 most presented species binary classifiers were trained. Among them only *Pimpinella tragium* models were selected for the further work due to their highest performance. R open source software was used solely to build and evaluate models based on various machine learning methods including maxent (implemented in «maxnet» R package) in a uniform and reproducible way. As it is known that correlated predictors usage lower model performance, in another part of the work we excluded several initial variables in order to reduce data dimensionality and statistical «noise». Indeed, certain Worldclim variables are bound to be highly correlated (i.e. maximum temperature of the hottest month and the hottest quarter, isothermality is a result of the division of one variable by another and therefore holds no additional information, etc.) Accordingly, we performed correlation analysis as well as principal component analysis (PCA) and were able to establish most correlated and less contributing to the dataset variance variables which were removed from the new reduced dataset. Lesser correlation of the new dataset variables was evidenced and hierarchical clusterization for the two dataset was carried out. The latter separated certain climatic regions successfully in both cases; the data reduction thus caused only minor changes. As a side note, the clusterization here might be usefull for automated demarcation of climatic regions in general case. Next, various supervised machine learning techniques were applied to train and evaluate binary classifiers for both datasets. The result suggests comparable predictions with better performance in case of models trained using the reduced dataset. In conclusion, various machine learning techniques used alongside with maxent as well as reducing predictor set (i.e. bioclimatic variables) by means of unsupervised machine learning appears to be beneficial for SDMs performance.

Complex of open access databases of Altai State University for the purposes of the Altai-Sayan ecoregion research

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Комплекс баз данных Алтайского государственного университета открытого доступа для целей исследования Алтае-Саянского экорегиона

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Ten years ago, to study the biological diversity of the Altai-Sayan Ecological Region (ASER), the process of developing and creating a set of open access databases on the Internet was launched in the Altai State University (ASU, Barnaul). To date, ten databases contributing the comprehensive study of the animal and plant world of ASER, have been developed. The databases were created using the web interface MySQL5 phpMyAdmin 3 and located on the server of ASU (ssbg.asu.ru). The mountain system of Altai and Sayan has a relatively small territorial area, but is the habitat of a large number of biological objects. In 2002, David Olson and Eric Dinerstein singled out this territory as one of the 200 priority ecoregions of the world for global conservation of biodiversity (Annals of the Missouri Botanical Garden 89: 199–224) in their work “The global 200. Priority ecoregions for global conservation”. Considering the data of 200 ecoregions, they noted that 90 % of the world’s biodiversity is concentrated on 10 % of its territory. There is an information on the most popular databases from the existing ones below. Biodiversity of the Altai-Sayan ecoregion (ASER) (bioaltai-sayan.ru). The database contains an information on the biological diversity of the ASER within the territories of Russia, Mongolia, China and Kazakhstan. The database reflects the current generally accepted systematic classification and is organized as a list of biological objects (animals, plants, mushrooms) that are represented on the territory of the ASER. The database contains the Russian and Latin names of the species, its distribution. Characteristics of the species include distinctive morphological characters, its place in the accepted classification groups by distribution (rare, endemic, etc.), as well as statuses in the Red Data Books of Russia, Mongolia, China, Kazakhstan and the IUCN list. For the most species, distribution maps and photographs are given. Virtual Herbarium SSBG (ALTB). The electronic

database of materials of the herbarium funds of ASU (Herbarium ALTB) is available on the Internet at www.ssbg.asu.ru/altb_herbarium.php. The structure of the database is presented as a catalog of species on the collections of ALTB, which is formed by drop-down lists (collection, family, species, country, herbarium status) for convenience of searching and sorting. A separate database record contains an image of the herbarium sheet (with an individual barcode number) and text information (label content), which includes 16 items. Checklist of lichens of the Altai Territory. The database is designed to store, systematize and search for information on the species composition of lichens of the Altai and its individual botanical-geographical regions, species included in the Red Data Books, as well as bibliographic references to publications in which this information is contained. For species included in the national or regional Red Data Book, the conservation status is indicated.

Concerning the problems of regional reference plots system for ground support of remote sensing materials processing

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К проблемам развития системы регионально верифицированных эталонов для наземного сопровождения ДЗЗ

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The landscape complexes state assesment, including natural and anthropogenically transformed ecosystems, is the basis for the organization of rational nature management and biological diversity conservation. A significant amount of space materials already accumulated and constantly

replenished can become the basis for a large-scale spatial and temporal analysis of the ecosystems current status and dynamics. However, an indispensable condition for this, in our opinion, is the support of remote sensing data processing by regionally verified materials of integrated ground survey at regional reference plots. Within them must be presented the reference plot blocks of different status (natural, disturbed, converted, regenerated). The existing methodology for the remote sensing materials processing, including the construction, training and testing of classifiers, the use of spectral indices, needs to be developed due to the "non-universal" nature of the vegetation and soil cover of the Earth. As the characteristics associated with species composition and vegetation condition become more detailed, the importance of ground-based measurement increases. Thus, recognition of the species composition of the tree layer, the practice of which is developed for forests in certain areas of South America, India, the USA, China, can not be extrapolated to ecosystems of other species composition. On the example of the forest-steppe - steppe Middle Povolzhye (Samara region) as an ecotone with a mosaic combination of preserved natural ecosystems, agro ecosystems, urban complexes, spontaneously recovering ecosystems, we can demonstrate the need for a network of regional reference plots for ground support of remote sensing data processing. An important point in its formation is to unite the efforts of specialists in various fields. Some of the experience we have gained in recent years in the development of steppe, forest ecosystems, former field deposits as reference plots has shown that one of the problems may be the availability of accessible space images of the desired areas with high resolution, closely timed to the required deadlines. In the near future, we plan to continue to collect ground information on the state of particularly valuable natural communities typical for the Samara region and adjacent regions on new reference plots, as well as the selection and cataloguing of satellite data reflecting diagnostic parameters and the time frame for their detection.

**Creation of electronic catalogue of big zoological
collections by example of collection of Onithological
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Оцифровка больших зоологических коллекций на примере сектора орнитологии Зоологического музея МГУ им. М.В. Ломоносова

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In 2018, employees of the Onithological Section of the Zoological Museum of Moscow State University completed the digitization of collection represented by stuffed and flat skins, as well as mounted birds. To date, all the Section's storage units that have inventory IDs have been included in a integrated single electronic database. The bird collection of the Museum is the second largest in Russia and is one of the twenty largest collections in the world. Digitization of this huge massive of information was conducted by staff members together with temporary assistants under the supervision of scientific staff. All the data were taken directly from the collection labels. The first 20 490 rows were added to the database in 2000–2014 during the new collections registration fresh cataloguing of the type specimens. Targeted work on the creation of a full database covered three years from January 2015 to December 2017. In the process of digitization, participants faced a number of problems. Some of them were: duplication of inventory IDs; determination of the accurate coordinates for the collection localities; the establishing of the correct surnames and initials of little-known collectors. The search and correction of uncertainties in the database records is still continues. Nevertheless, we can report significant results of the work even now. The species identification of several hundred birds was refined or processed de novo. The exact number of storage units of the Section was determined precisely: at the moment of the end of May 2018 there are 129 979 specimens including 2 193 downy chicks excluding birds of the permanent Museum exposition, and those sent somewhere for exchange. Twenty one specimen represent extinct or probably extinct taxa. The most notable sources that formed the Museum funds

were collections of G.I. Langsdorf, M.M. Berezovsky, V.N. Bostanzhoglo, G.I. Polyakov, S.A. Buturlin, V.A. Khakhlov, V.M. Gudkov, as well as the material collected by Museum staff during different years. The creation of the network database with parallel access for several operators based on MySQL server became an important frontier in the work of the Section, after which many of the usual operations were accelerated and optimized notably. For the purpose of accessibility for specialists from around the world, the database is published on the official website of the Museum and in biobank of the Moscow State University. Currently, a portion of the database for the collection of bird tissue samples, which are the source for DNA extraction is being completed. In the nearest future we are planning to digitize collections of alcohol preserved materials and clutches, as well as publication of articles involving data from the electronic catalogue including the catalogue of type specimens. The work was carried out with the financial support of the RNF grant № 14-50-00029 “Scientific foundations for the creation of a National Depository Bank of Live Systems”.

Creation of Information retrieval system on the unique research collections of the Zoological Institute RAS

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Создание информационной системы для уникальной фондовой коллекции Зоологического института РАН

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Zoological Institute of the Russian Academy of Sciences (ZIN) — one of the oldest scientific institutions in Russia with unique scientific collections. In 2017, the Museum and the Institute celebrated their 185th

anniversary. The unique collection of the ZIN were collected by many generations of Russian and foreign zoologists throughout the territories and waters of our planet. Collected during these expeditions materials are stored in the Institute, they remain imperishable source of information on the structure and distribution of faunal diversity in space and time. The collections continue to rise. ZIN has one of the largest zoological collections in the world, with more than 60 million of storage units. In general, in the collections of the ZIN about 260 thousand species of animals, which is about a quarter of the known world fauna, are presented. There is almost all the animal species inhabiting territory and waters of Russia, for many of them the big series are stored. Several tens of thousands of type specimens of animal species stored in the collection are of exceptional value. The content of the concept of “zoological collection” in our days of rapid progress of information technologies and advances in molecular genetic studies quickly filled with new meanings. Currently, the collection is rightfully regarded as a bank of scientific information and the primary tool for basic and applied biological research. The information system should include taxonomical, type, collection, zoogeographical and bibliographic data. By using of available server infrastructure of ZIN and information system of collection specimens created (ZIN Research Collections portal, <https://www.zin.ru/collections/>), there was a possibility of selective publication of ZIN research collection data via GBIF portal (<http://ipt.zin.ru>). The scientific use of the collections and depositories of integrated information systems for faunistic biodiversity in the present context includes, as the most important modern goals, digitization of collections and publication of information in the public domain on the Internet as well as the creation of a DNA bank. Work is carried out within the limits of researches on a theme “Inventory of a biodiversity of animals and its supply with information” (AAAA-A18-118012990224-5) and partially carried out at support of grants of the Russian Foundation for Basic Research № 15-04-02971 and № 15-29-02457.

Data base “Herbarium KLGU” by IKBFU

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База данных “HERBARUIM KLGU” БФУ им. И. КАНТА

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The Herbarium of the IKBFU, which are registered in the international database Index Herbariorum (KLGU), was created on the base of natural-historical faculty of KSPI in 1964. The research collection started to add up in the late sixties in XX century. The collection of the herbarium samples of IKBFU includes about 50 000. The main part of them (nearly 48 000) is fond ones. The herbarium for students' education contains about 25000 samples. Also, there're ones from different regions of Russian Federation and from the abroad. The collection of the herbarium samples is kept in the special metal cabinets. The main organization level is bloodlines, species in alphabetical order. The data base “HERBARUIM KLGU” is based on the SQL Server 2014 Management Studio platform, software code - Microsoft Visual Studio 2015 with use of ASP .NET MVC 5 (Petrenko, 2017). In the process of the initiate specimen selection for scanning the exsiccate herbarium samples “Saint-Petersburg flora” (by K. Meinshausen, Herbarium Florae Ingricae) were spotted. The samples from this collection appeared in the KLGU fond in consequence of exchanging with St. Petersburg University (SPbU). The samples are dated back to the latter half of 1860s. Also, these ones have original labels written with quill. Nowadays, about 2 000 samples have been scanned. The herbarium samples of Orchidaceae Juss family and part of collection by K. Meinshausen are form the mainstay of the digitized herbarium (Gusha, 2018). Work is underway to adding up information of the herbarium sample including 600 dpi and 1200 dpi scanning resolution. For now, the main unsolved problem is user-friendly interface creation for nonprofit. The herbarium data base users. A herbarium data base advantage is that not as bulky as other herbarium data base, in spite of its tier system. To give rein to nonpro users, using only the sitxth sense, find needed information of the herbarium sample. For another thing, ability to print a QR-code with extra information for more convenient code reading and processing information by users.

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Database of Barguzinsky reserve

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Базы данных Баргузинского заповедника

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ФГБУ “Объединенная дирекция Баргузинского государственного природного биосферного заповедника и
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One of the objectives of the reserves is to maintain a long-term monitoring of natural complexes' state. Barguzinsky Reserve, being the oldest in Russia (organized in 1916) and located on the northeastern coast of Lake Baikal, is a standard of unspoilt nature that reflects biota responses to global climate change. Regular observations of natural objects and phenomena in Barguzinsky Reserve cover the period from the late 1930s. Currently there is a continuous dataset of observations for 30-60 years. This data contains: inventory lists of flora and fauna; the results of accounting for the number of major species of ground beetles, mammals and birds; an assessment of the yield of berry and tree species; phenological observations and climatic data series; observations of populations of rare plant species. The data is stored in 25 databases. All available materials were used as a source for databases, including published data, primary observation files, manuscripts of Nature Annals, and other unpublished reports. Digitization of data makes possible to systematize the primary

observation materials available in the reserve, to facilitate access to them, to preserve these observations from loss, and to perform an inter-related analysis of long-term series of observations. At the moment inventory lists of higher vascular plants and herbarium of the Barguzinsky Reserve are being prepared for publication in GBIF.

Data lineage for Baikal microbiome study

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Отслеживание происхождения данных в исследовании микробиома Байкала

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The Baikal microbiome study is being conducted in Limnological Institute of SB RAS, the study is based on the next-generation sequencing data analysis. As a result, the study generates a big volume of metagenomic data. The work considers issues of the data lineage for Baikal microbiome study with the next-generation sequencing, from a moment when researchers describe a sample of water or bottom sediments to publication of research results. We propose a service for data lineage based on storage and execution of metagenomic processing and analysis pipelines. The service provides reliability and reproducibility of published research data.

Development of regional biodiversity portal in Khanty-Mansi Autonomous Okrug-Yugra

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Разработка информационного портала “Биоразнообразие Югры”

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Khanty-Mansi Autonomous Okrug – Yugra located in the central part of Western Siberia. Biodiversity-related studies are relatively young there in line with intensive industrial development of the region in recent decades. The region poses a few of biological collections within the Universities and Nature Reserves. Still, the Department of Natural Resources of Yugra pays considerable attention to the sustainable use of natural resources. The advance of computer and Internet technologies produces response in biodiversity science, thus biodiversity informatics discipline developing quickly over last decades with considerable results in development of protocols, standards and global platforms for integration of biodiversity data. The data flow from local, regional and national nodes to global platforms (like GBIF) where integrated data are broadly available. On the local scale, the employment of biodiversity informatics methods for storage, analyses and publication of biodiversity data greatly improves the quality of work. Organization of biodiversity portals promotes education and opens the realm of science to citizens. Due to these reasons organization and development of biodiversity portal in Yugra region would be an important and timely task. Previous experience of biodiversity information systems in Yugra was only initial. The program on digitization of observations of Red Listed species was launched in 2010 under support of the Department of Natural Resources. The information system UGRABIO developed through this project currently includes about 3 thousand observations. Another case of digitization was shown by a biological collection of Yugra State University with its database based on Specify product and available online through its web version. Some collections of Nature Reserves have their catalogues in digital form. The demand of collections digitization seems well understood as shown at regular workshops on Biological collections management held in Khanty-Mansiysk. Recently biologists curating several biological collections in the region started a project on a regional biodiversity portal (YugraBio). The already developed product Symbiota – a package of web tools for integration of separate collections databases will be used for the portal development. The YugraBio project will include several stages: 1)

a metadata database of biological collections in Yugra will be developed, 2) major biological collections will be digitized, 3) algorithms and guidelines will be developed during the digitization, 4) the overall structure of the portal will be developed, 5) the portal will be linked to the national IPT node for export to national and international (GBIF) portals, 6) finally the workshops and seminars for information dissemination should be organized. The collected massive of data in the portal would give new opportunities for biodiversity research and sustainable management of nature resources in the Yugra region.

Development perspectives of CRIS

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Cryptogamic Russian Information System - CRIS (<http://kpabg.ru/cris>) is devoted to cataloging biodiversity information of the cryptogamic organisms such as algae, fungi, lichens, and bryophytes. In contrast to Darwin-Core principles with its single species record as a baseline, CRIS is working with multispecies records. CRIS allows for users to enter different types of data such as labels of herbarium specimens, literature references, media files etc. Rapid increase of records number, diversification of types of materials, complication of the structure of the record forced us to switch from CMS Drupal to modern Node.js. The major problem in CRIS is to fix issue related to slow geo-searches, which are overloading server at the moment. Mass processing of data and other features will be convenient improvements of the system. The modified version will have intergroup search; this will be accomplished by making connection between different sections of CRIS. In contrast to the old version of the CRIS based on Drupal, new version will have universal numbering system with “Universal herbarium specimen” (UHS) as a core. UHS from one herbarium may be easily converted into record of another herbarium, when for example

curator is sending specimens to another herbarium physically or give them for the loan. The new version offers option to entering information about distantly related organisms for examples cyanoprokaryotes and diatoms in single record. By the end of the testing period, new groups of organisms such as vascular plants, diatoms, protists and fishes will be included in the new version of CRIS. Eventually, CRIS will have new abbreviation, which is Complex Research Information System. The main result of this project will be development of modern, online IS, which is not attached to the local computer. That system will provide quality free access to biodiversity data. The release of the new version of the CRIS announced for December 2018. This study was conducted with the partial support of grants from Russian Foundation for Basic Research (projects № 15-29-02662, 18-04-00171, 18-04-00643).

DINA. An Open Source web-based collection management system for natural history specimens and for publishing data at GBIF

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Swedish natural history museums and collections house more than 33 million objects from all over the world out of which 10-20% are digitized and published by the Global Biodiversity Information Facility (GBIF). This huge backlog of more than 25 million objects is problematic in itself. In addition, the specimens already digitally available were until recently locally curated and presented by a multitude of home-grown and commercial systems. To remedy the inconsistencies in using different collections management solutions, a decision was made during 2014 to establish a consortium aiming to address these problems by developing a single, unified Open Source web-based system for collections management – DINA (“DIgital Information system for NATural history data”, <https://dina-project.net>). This presentation will give an overview and significant details of the structure, development and present status of the DINA web-based collection management system. The national Swedish DINA consortium is governed by a steering group where all the major natural history museums in Sweden

are represented. The main responsibility for DINA systems development is located at the Department of Bioinformatics and Genetics at the Swedish Natural History Museum in Stockholm. There is also an international consortium involving several partners in Europe and North America adopting DINA modules of their choice, and more collaborating partners are subsequently invited. Currently the core team of developers in Stockholm consists of a project manager, four developers and two domain experts. The expected timeline for presenting the first pilot collections is due by the end of 2018. DINA is designed as a loosely coupled set of web-based modules, based upon a compilation of comprehensive guidelines for web service application programming interfaces (APIs) ensuring interoperability of modules. All DINA components can be modified or even replaced by other components as long as they are DINA compliant. Furthermore, the modularity enables the institutions to host only the components they need. These features will all be described herein, as will the step-by-step SCRUM working process (reference groups – one collection at a time; focus on the data model; continuous collaboration between domain experts and developers). Finally the data-publishing components enabling automatic transfer of data to GBIF – including using TDWG standards (e.g. DwC Archive) will also briefly be touched upon.

Distribution of endemic locoweed species around lake Baikal

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Mountainous regions of Siberia are characterized by high diversity and endemism of locoweed species. Within Siberian regions Baikal hemiboreal floristic province has a big number of endemic *Oxytropis* species. This phenomenon can be connected with mountainous landscape and long-term isolation of steppe patches on territory around Lake Baikal. Many of endemic species on this territory are recognized as rare and endangered and detailed studies of their distribution will contribute to future conservation activities. Distribution models were generated using Maxent (Version 3.3.2k). Georeferenced plant occurrence data were accessed from herbar-

ium collections and results of own studies. We used 19 bioclimatic variables with resolution of 0,5 arc-minutes (www.worldclim.org). All models were statistically tested, jackknife test were used to reveal the importance of variables. Distribution analysis showed that the most part of endemic *Oxytropis* species localities confined to the mountainous regions on the south of Baikal Siberia. Analysis showed high diversity and a big number of localities of endemic locoweed species in Buryatia. Main part of studied species on the territory of Irkutsk region can be found at the Eastern Sayan mountains and Tazheran steppes (near Olkhon island). Endemic locoweed species in Zabaikalskii krai concentrated in Aga steppes, Kodar ridge, Chara depression, and Sokhondo nature reserve. The most part of studied species characterized by narrow fragmented distribution with small quantity populations. More than half of studied endemic locoweed species (13 from 23) are included to regional Red Data Books. Distribution of *Oxytropis glandulosa* revealed to two main clusters: one in the Barguzin depression, second – around Eravna Lakes. Bioclimatic modeling didn't show new habitats suitable for this species. New localities can be found within current species distribution. Important variables for this species are BIO7 and BIO9. *Oxytropis bargusinensis* mostly occur on the northern part of Baikal Siberia. Potential distribution for this species under bioclimatic modeling included southern part of Buryatia (valleys of rivers Selenga and Uda). Here also temperature variables (BIO1, BIO7, BIO9) have big importance on species distribution. Research was carried out under the project granted by the Russian Foundation of Basic Research (№16-04-01399) and Federal Budget (project № AAAA-A17-117011810036-3)

DNA-barcoding in the study of rare plant species of Belarus

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Использование ДНК-штрихкодирования в изучении редких видов растений Республики Беларусь

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Among the main environmental challenges of our time, the ones associated with decline of species diversity and a decrease in the areas of natural ecosystems stand out. The Republic of Belarus has made a significant effort to conserve and sustainably use biological diversity. The mechanisms that provide for the maintenance of specially protected natural areas and the Red Book of the Republic of Belarus are worth noting among the effective instruments enabling the preservation of environmental objects. Beyond that, environmental activity entails an inventory, mapping of locations and cataloging of rare and endangered species of plants and animals. A key milestone in ecological monitoring was the establishment in 2013 of the Republican DNA Bank with its collections that constitute a depository of biological material apt for long-time storage. The scientific activity of the Republican DNA Bank is based on the molecular-genetic identification of species and verification of their taxonomic status which offers ample opportunities for collaboration in such a priority direction as DNA-barcoding. DNA-barcoding is a widely used technique of genetic data digital representation convenient for cataloging and storing of information on molecular features of living organisms' genomes. The use of certain nucleotide sequences (DNA barcodes) in biosystematics allows to accurately identify the species under study, compare related genomes, and effectively manipulate large arrays of genetic data. As of now, the Republican DNA Bank employees have performed research on 35 rare and endangered plant species (I-IV protection categories) collected in the National Parks "Narochansky" and "Belovezhskaya Pushcha". The biological material of rare plants was collected without removing them from their habitat. Classical methods of botanical research along with simultaneous compilation of a database on morphological and ecological geographical descriptions of every plant preceded the molecular-genetic analysis. Polymorphism of three marker sequences ITS2, *rbcL*, *psbA-trnH* was used for DNA barcodes identification. All the information obtained is uploaded to the website of the National Coordination Centre on Access to Genetic Resources and Benefit-sharing. With the involvement of the Republican DNA Bank, a DNA Barcoding Centre, containing a barcode database of flora and fauna of the Republic of Belarus, is being established. The Centre will consolidate research institutions and universities which have natural science collections and environmental institutions of the Republic.

DNA barcoding of *Waldsteinia* Willd. (Rosaceae) species based on ITS and trnH-psbA nucleotide sequences

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ДНК-штрихкодирование видов *Waldsteinia* Willd. (Rosaceae) с использованием нуклеотидных последовательностей генетических маркеров ITS и trnH-psbA

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In our study, we estimated the Internal transcribed spacer region (ITS) and trnH-psbA intergenic chloroplast spacer as possible markers for species identification of vascular plant genus *Waldsteinia* (Rosaceae). The comparative analysis of the nucleotide sequences of East Asian *Waldsteinia maximowizii*ana, South Siberian *W. ternata* and *W. tanzibei*ca, European *W. geoides* and *W. trifolia*, North American *W. fragarioides* and *W. parviflora* was carried out. PCR was performed using both GoTaq Flexi DNA

Polymerase kit supplied with green buffer (Promega) and Q5 High-Fidelity 2X Master Mix (New England BioLabs). PCR products were visualized on 1.5% agarose gel with ethidium bromide upon electrophoresis, gel-purified using the GeneJET Gel Extraction Kit (Thermo Fisher Scientific), ligated into pTZ57R/T (Thermo Fisher Scientific) or pMiniT 2.0 (New England BioLabs) plasmid vectors followed to cloning in TOP10 *E. coli* competent cells or directly sequenced. Bacterial cloning was used for detection of low copy number variants of ITS region. Isolated plasmids and original amplicons were sequenced by Sanger method using BigDye Terminator Cycle Sequencing kit v. 3.1 (Applied Biosystems) on the 3500 Genetic Analyzer (Applied Biosystems). From two spacers of ITS region for molecular identification of plants using BOLD system ITS2 region is recommended, however, our data showed a high intraspecific and intrapopulation variation of this region, together with a low number of systematic substitutions do not allow distinguishing of closely related species. Thus, using of ITS2 region as a molecular marker for *Waldsteinia* spp. is very ambiguous. The detected levels of intra- and interspecific ITS1 and trnH-psbA variability allow using these molecular markers for identification of *Waldsteinia* species. The best results were observed in case of combining the ITS1 and trnH-psbA sequences together, which allowed to identify species in 100% cases according the ‘best close match’ test. The study was supported by the Russian Science Foundation (project No. 17-74-10074) and the Russian Foundation for Basic Research (projects No 16-34-60135_mol_a_dk and 16-05-00783). The research was done using the equipment of The Core Facilities Center “Bioanalitika” and collections of The Core Facilities Center “Bioresource Center” at Siberian Institute of Plant Physiology and Biochemistry SB RAS (Irkutsk, Russia), IRKU, IRK and LE herbariums and Botanical Garden of Irkutsk State University.

Electronic database of the collection of living microalgae strains and cyanoprokaryotes of the northeast of the European part of Russia

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Электронная база данных коллекции живых штаммов микроводорослей и цианопрокариот северо-востока Европейской части России

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Electronic database was created to maintain the collection of microalgae living cultures was started in the Institute of Biology (IB) of Komi Scientific Centre in 2010 as a part of IB SYKO herbarium (<https://ib.komisc.ru/sykoa>). The collection is egistered in GCM (Global Catalogue of Microorganisms) Acronym: SYKOA, WDCM Number: 1125. Today, the collection contains more than 300 algologically pure strains of algae collected in the European Russian Northeast (Polar and Subpolar Urals, Bolshezemelskaya tundra), isolated from soil and water samples. Also, there are several strains from soils of the Southern Svalbard and other Arctic regions. Green algae and cyanoprokaryota/cyanobacteria form the main part of the collection. Departments Eustigmatophyta and Xanthophyta are presented in the collection by five species. Collection includes monocultures of dominant species of algae from different ecological groups (edaphophilous, cryophilous, nitrophilous, etc.), rare species and taxa with uncertain systematic position. The main aims of the collection are to conserve biodiversity of microalgae from Arctic and northern regions of the European Russia, and to collect new strains for their use in floristic, systematic, evolutionary, molecular, genetic and ecological studies.

Experience in the use of GIS tools in plant systematics and conservation

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“Опыт использования ГИС-технологий в сиситематике растений и охране природы”

The ecological niche and the range are sufficient characteristic of the species. In turn, each species has its own unique ecological niche, ecoclimatic characteristics to be its important component. The MaxEnt algorithm allows not only to obtain a species distribution model, but also to evaluate it, using the AUC. It is also possible to estimate the impact of each bioclimatic variable on the model. The SDMtoolkits (Brown, 2014) on one hand, allows to spatially rarefy the input data at several distances according to habitat, topographic or climatic heterogeneity. As far as the breath of area, covered by analysis, depends on latitude, being larger at equator and the smallest at poles, the data of occurrence, prepared for MaxEnt, should be biased. SDMtoolkits resolves this problem as well. On another hand, it can evaluate the correlation between bioclimatic variables, and exclude the highly autocorrelated ones from being incorporated, and avoid the mistakes in evaluation their contribution in the model. The impact of variables can be evaluated in three independent ways: direct contribution (in percent), revaluation after permutation, and with jack-knife test. The opportunities provided by the climate modeling programs Bioclim and MaxEnt, as well as the SDMtoolkits and ENMTools applications, were implemented in our study of bluegrasses (*Poa* L.). Using freely available climatic data and the data of occurrence, the bioclimatic profiles of morphologically similar *Poa palustris* L., *P. nemoralis* L. and populations, combining the characters of their both, treated as Aggr. *P. intricata* Wien., were revealed, using the Bioclim program, implemented in DIVA-GIS. The models for their potential distribution in the current climate, in Pleistocene maximal glaciation, in interglacial and the Middle Holocene were reconstructed with MaxEnt and applications. The comparison methods - niche-identity test (I-test), and background test (B-test), implemented in the ENMTools program, make it possible to compare the obtained ecologo-climatical niches. The I test allows to reveal a statistically significant difference between the niche models, calculated for different taxa, and the second one allows to establish the divergence of niches at the genetic level, which makes these methods an important tool for study the divergence, speciation and microevolution. We compared the ecologo-climatical niches of all three species, and I-test has revealed their differences at a statistically significant level. The models of potential species distribution, constructed on the basis of ecologo-climatical niches can be

used not only for paleogeographical reconstructions, but also are of a great practical value. They allow predicting the expansion of invasive species, the possibility of the useful species introduction, the probable dynamics of ranges in accordance with various scenarios of climate change in the future and reveal the possible locations of rare species.

Flora Pomeranica Orientalis – a way to store floristic data of Gdanskie Pomerania

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For many years scientists were trying to figure out how to unify and visualize data on plant range. It started around 1970s, with Hulten and Meusel, and went on from there, still being developed. To make it more accessible, in 2000 arose GBIF, one of the most complex online databases. Due to special meaning for Gdanskie Pomerania, as the area where the ranges of many plant species overlap, with a great diversity of natural habitats, interesting geological history and the relatively poorly understood distribution of species, there was a need to create such an initiative in this region. Pomerania is very important in terms of phytogeographical area of Europe, where the boundaries of the areas of many taxa meet, eg with the (sub)Atlantic, continental or southern European type of range. It is also relatively well preserved in naturalistic terms. The sea coast is rich in young glacial types of landscapes, numerous wetlands, peat bogs, lake and river ecosystems, including the estuary of the great river - Vistula and Oder. Floristic data in this area has been collected for over 150 years, at first by German botanists and naturalists, and after 1945 – Polish ones. Unfortunately, they have not yet been unified, even though they were partly used in the work on the Atlas of distribution of vascular plants in Poland. Large scale of a single cartogram unit adopted for a nationwide study (100 km²) did not require the use of all data and is not enough for solving phytogeographic problems in the scale of the region. In 2006, the Westernpomeranian Atlas of Distribution of Vascular Plants and Mushrooms (ZARRiG) was created, which purpose is to supplement and summarize knowledge about floristic and mycological resources of north-

western Poland, based on available historical and current data. In 2017, Flora Pomeranica Orientalis was founded, covering the area largely coincides with the area of the Pomeranian Voivodship, as well as with the geobotanical region defined as the Gdansk Pomerania. Flora Pomeranica Orientalis is a project held by the Herbarium of the University of Gdansk – Herbarium Universitatis Gedanensis UGDA from the Department of Plant Taxonomy and Nature Conservation, University of Gdansk. It was established in cooperation with the creators of the Westernpomeranian Atlas. The main goal of the project is to collect and archive floristic documentation from the area of Gdansk Pomerania in a database, which unifies the format for storing floristic data from different authors, and thus is to be a tool enabling the integration of many separate botanical datasets into one system. Project aims to improve the exchange of scientific information and the results of fieldwork between data authors. The database allows users to collect and edit their own data, as well as to share data with other users. What is important, all data entered and stored in the system are protected by copyright.

Forest fires and landscape changes in protected area on the northeastern shore of lake Baikal

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Природные пожары и изменение ландшафтов на ООПТ северо-восточного побережья озера Байкал

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There are three large Federal Protected Areas the northeast shore of Lake Baikal: Barguzinsky State Nature Biosphere Reserve, Zabaikalsky

National Park and Frolikhinsky Wildlife Sanctuary. All of them are managed by the Federal State Establishment “Zapovednoye Podlemorye” providing the strictest status of protection. However natural forest fires have had great impact on landscapes and their components. Crown and ground forest fires of various intensity have burned vast areas of subalpine, forest and coastal landscapes over the past three years. Current conditions of damaged landscapes allow us to conduct assessment on the process of ecosystems recovery. Geosystem approach is applied to define of landscape types and landscape (land cover) and map them; to assess burned area and to consider changed in vegetation on monitoring plots. The Shumilikha valley in Barguzinsky Nature Reserve serves as the case study area. Here coniferous forest landscapes were damaged in 2015. With the use of the satellite images and results of monitoring on plots, pace of landscape recovery can be modeled for the site and territories of three protected area.

Forest resources of the Baikal region: vegetation dynamics under anthropogenic use

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Лесные ресурсы Прибайкалья: динамика растительности при антропогенном использовании

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We review the theoretical and applications-specific issues of the modeling the temporal and spatial dynamics of forest ecosystems, based on the principles of investigating dynamical models. The model used takes into account various factors affecting the change in forest areas - fires, forest

diseases, cutting, urban expansion, etc. Calculation of numerous scenarios for the use of forest resources makes it possible to see the consequences of various managerial decisions. The user can access the parameters of the main cutting volume, fires and tree planting. We present the results of a computer modeling and predictive mapping for the regional model under anthropogenic use of the forest resource dynamics.

Fractal models for assessing the functional diversity of organized soil microbial communities

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Фрактальные модели для оценки функционального разнообразия организованных почвенных микробных сообществ

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Soil microbial communities regularly self-organize to implement joint biochemical reactions and extract necessary nutrients from plant substrates. When changing substrates the configuration of the microbial biosystem is automatically rearranged evenly distributing the enzymatic load between the microbial components. In article proposed to use fractal

models of frequency-taxonomic specter of microbial communities to assess the functional diversity of the processes of self-organization of microbial communities. The proposed mathematical methodology based on a fractal analysis of the location of operational-taxonomic units (OTU) of microbial communities on a two-dimensional fractal portrait of these communities. Initially, the original OTU spectrum converted into a reduced spectrum of OTU groups, in which each group combines individual OTUs that are similar in frequency. On a two-dimensional fractal portrait of the microbial community, each OTU group represented by a point with coordinates that depend on the frequency of occurrence of this group. As a fractal measure, in the analysis triangles with vertices at the points of OTU groups are used. In this case, the smallest height of the triangle chosen to be the scale of the fractal measure. The construction of triangles and their arrangement in order of increasing scale of the fractal measure allows us to identify the first triangles, which are degenerate triangles. Degenerate triangles on the portrait of the microbial community unite the OTU groups that are in the biosystem. The share of biosystemic OTU groups in the microbial community determines the scale of the joint participation of soil microorganisms in biochemical reactions (IFS is the index of fractal structures). The taxonomic composition of biosystemic OTE groups determines the functional orientation of biochemical reactions in soil microbial communities. When analyzing the molecular genetic data of soil samples, which moistened with pure water and exudates of rye and wheat, the values of IFS for these samples were calculated out (0.48, 0.50, 0.52, respectively). On the this basis, it can be argued that plant exudates play an important organizing role in the development of plant-microbial interactions.

GBIF (Global Biodiversity Information Facility): Example of a national node (France) and actions at Regional level (Europe)

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GBIF—the Global Biodiversity Information Facility—is an international network and research infrastructure funded by the world’s governments

and aimed at providing anyone, anywhere, open access to data about all types of life on Earth. Over 976 million of biodiversity data from over 1170 institutions worldwide are now accessible through the GBIF portal (www.gbif.org). The national GBIF nodes promote the GBIF activities at national and regional levels and help to mobilize the data. This presentation will show an example of implementation in France. GBIF France animates, federates and brings its technical support at national level. It was set up in 2006, with a dual mission: to represent GBIF in France, by providing French scientific and political communities with the tools and services created by GBIF; and represent France in the GBIF. At Regional level, we organise a European Nodes meeting, each year, to discuss potential actions that can be done jointly, in order to raise the mobilisation and uses of the data at a larger scale. This presentation will present the current contribution of European nodes in GBIF and exemple of common actions.

Geographic information system "Bryophyte diversity in the Republic of Bashkortostan"

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ГИС-система "Разнообразие мохообразных Республики Башкортостан"

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Experience about results of grid mapping, relevant to bryophytes in Great Britain and other countries has showed possibilities for solutions, that covers a wide range of questions about biology and ecology of species, as well as role of different ecological factors in form of diversity and distribution of separated species, also objective rating their rarity and protection needs. Based on consolidation results of inventory bryophytes an electronic atlas of «Bryophyte flora of the Republic of Bashkortostan» is created. In

this atlas location of species is showed as square polygons in layers. It designed for displaying in different scale of the map. Application is built with using open source software like DotNet Core, GeoServer, PostgreSQL with PostGIS extension. LeafletJS library is using for displaying spatial data. DotNet Core is used for web-based application. The main part of spatial data is stored in PostgreSQL database with PostGIS extention. Geoserver is displaying spatial data for vector and raster data. Layer's style is supported with Styled Layer Description (SLD). Main page consist of « Bryophyta» and « Marchantiophyta». Each of them is navigated to list of species. There is a page where contained link to source of species finding in the Republic of Bashkortostan, a list of synonyms, photo and location species on map of Bashkortostan with scale 1:5000000. The page consist 4 information links: "Ecology", "Conservation value", "Bibliography" and "Detailed species location on RB". "Ecology" page consists of species's location description and 3 charts: "Occurrence within alliances of floristic classification of vegetation», «Occurrence in EUNIS habitats» and «Elevation range». "Conservation status" page consist information about on the needs to protect the species. "Bibliography" - list of publications. When «Detailed species distribution within Republic of Bashkortostan» is selected, two polygon layers of species are downloaded, which is compiled from polygon grids in WGS84 geographic system and base tile map (by default Open Street Map (OSM) tile layer). Square's size of first layer is 6' long of latitude and 10' long of longitude (10x11km) which equals with a lot of similar European resources. Second polygon layer contains polygons which are divided to 100 pieces (36" long of latitude and 1' long of longitude). This layer is designed for more detailed researches, for instance, within protected areas. When the square is selected in polygon layers we can see links to Bibliography about that species in current square, characteristics of habitat, person who collected data, the date of collecting. Geographic information system will be developed and modernized for creating atlases of rare plant species and plant community. It can integrate knowledge about bryophytes of the Republic of Bashkortostan in Russian and international databases, which turned up relevance of results regional and national bryological researches.

Geoinformational web-system for the analysis of the expansion of the Baikal crustaceans of the Yenisey River

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Геоинформационная веб-система для анализа экспансии байкальскими ракообразными реки Енисей

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Nowadays, it is generally recognized that the problem of biological pollution is one of the most important global environmental problems of our time, it is also actual for the The Yenisey River. Invasions of alien species in new ecosystems lead to significant changes in reservoirs - recipients, in particular, to a decrease in species diversity and the stability of aquatic ecosystems. It is known that the damming of the Yenisey caused a radical change in the hydrological, hydrochemical and hydrobiological regimes, especially in the afterbay of the Krasnoyarsk hydro-electric power station. Large-scale rearrangements have also occurred in the communities of benthic invertebrate animals - zoobenthos, which is the main food resource for most species of fish in Siberian rivers. At the same time the species diversity of bottom invertebrates has decreased significantly, but their number has increased. The increase in figures has been caused, first of all, by the distribution of endemic amphipods (crustaceans) from Lake Baikal through the Angara River upstream of the Yenisey. The paper presents modern quantitative data on the distribution of Baikal amphipods in the Yenisey River from the head to the delta inclusive, collected during field work in 2015 - 2016. The results of hydrobiological studies has been designed in the form of geospatial database in the geoportal, which gives the possibility to visualize and process geodata, and gives access to it from third-party applications based on cartographic web services. At this stage of the research, information on the hydrography of the Yenisey River basin was updated.

On the basis of the data from the geoportal, prepared in accordance with the State Water Cadastre, geo-referencing of the hydrobiological monitoring observation points to kilometer points along the fairway of the Yenisey River was carried out (“coordinate system of the river”); the use of such a coordinate system makes it possible to evaluate various parameters along the course of a river. Also, a set of specialized layers of geospatial data was formed. Creation of a geospatial database with the results of expeditionary work and the introduction of a geoinformational web system for information and analytical support of hydrobiological monitoring greatly expands opportunities in the analysis and representation of geodata, forms the basis for interdisciplinary research.

Geoportal monitoring system for the parameters of inland water bodies

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Геопортальная система мониторинга параметров внутриконтинентальных водных объектов

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The description of the geoportal monitoring system for the parameters of the inland water reservoirs of Siberia is presented. The information base of GIS is the optical and radar data of Earth remote sensing received from spacecraft Landsat-8, Sentinel-2 and Sentinel-1, as well as data from ground-based measuring complexes and expeditionary works. The GIS architecture, main modules and components are shown. The technological features of the work, the sequence of data processing and visualization are discussed. The results of using this system in the task of comparing the summer expeditionary data for measuring the concentration of chlorophyll “a” in the surface layer of the Novosibirsk Reservoir and the drainless

Krasilovskoe Lake with the value of the NDCI spectral index calculated from the data of the Sentinel-2 spacecraft are presented.

Geoportal of ISDCT SB RAS

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Геопортал ИДСТУ СО РАН

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Within the report, a technology is proposed for creating a geoportal for the collection and exchange of data between subject specialists. The technology is based on the developed model geoportal that implements common functions for many information systems. The technology significantly accelerates the creation of a subject-oriented geoportal that implements a ready-made set of various functions.

Global Biodiversity Information Facility: development goals and update 2018

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Глобальная Информационная Система по Биоразнообразию: приоритеты развития и новости-2018

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Global Biodiversity Information Facility (GBIF) aggregates data arranged in datasets, which are shared by a global and growing network of publishing organizations, such as natural history museums, citizen science organizations, and other institutions. Datasets are openly available from GBIF.org at four levels of information richness: i) metadata, or data descriptors, ii) checklists, such as national, regional or thematic lists of species, iii) occurrence datasets, which include location information for the records, and iv) sampling event datasets, which document occurrences together with sampling effort information and often with quantitative parameters of collecting events and observations. The steady growth of data content, improvements of GBIF.org and other tools translate into the increased and improved data use in science and policy. Often overlooked or treated as a negligible technicality, data play an important role at all stages of the scientific process from ideas, planning projects and funding to collecting, storage, publishing, sharing, analyses, presentation, discovery, repeatability and reuse of findings. Biodiversity sciences and policy increasingly become data intensive and dependent on availability and accuracy of the species occurrence data, accurate and unified nomenclature and sequence references, documented sampling efforts and standardized methodologies, and links among different data types. Linking traditional biodiversity data – location, time, names, images – to environmental, climate, interaction and molecular data is not trivial and is one of the main subjects of discussions by the GBIF, Biodiversity Information Standards (TDWG) and the related communities. GBIF encourages data capture and open data sharing using international data standards. DOI based mechanism of data citation ensures credit to the data originators, and therefore recognition of the field and database efforts and products as of first-class scholarly progress. GBIF strategic plan 2017–2021 is built around five priorities: i) empower global network, ii) enhance biodiversity information infrastructure, iii) fill data gaps, iv) improve data quality, and v) deliver relevant data. Implementation is carried out at three primary levels: global, participant, and data publisher. The presentation will present status, progress and plans as of September 2018, with the specific focus on collaborative opportunities for the individual researchers and teams, institutions, and countries.

Ground surveys vs. UAV photography: the comparison of two tree mapping techniques

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Nowadays, due to the rapid development of light-weight unmanned aerial vehicles (UAV), a remote sensing systems of ultra-high resolution became available to many researchers. The aim of this investigation was to compare the classical method (“from below”) and the newest one, using aerial images-based method (“from above”). Our field works were carried out in Prioksko-Terrasny Natural Reserve (Moscow region, Russia) on permanent sampling plot of 1 ha (100x100 m). A total of 779 trees with DBH at least of 5 cm were measured during ground survey in 2016. Species and Kraft’s class were determined for each alive tree and the radii of crown horizontal projection in four cardinal directions were measured. Crown projection of each tree was represented as a union of 4 quarter-ellipses, and the total area of all projections was calculated. The aerial photography by a quadcopter DJI Phantom 4 was conducted in 2017 on August, 2 from altitude of 58 m and on October, 12 (68 m). The orthophotomaps composed by means of DroneDeploy service (<https://www.dronedeploy.com/>) were used for manual vectorization of visible crown projections in Quantum GIS 2.8 software. For comparison we used only alive trees of upper canopy (1, 2, and 3 Kraft’s classes). Total area of tree crown projections according to ground-based tree mapping was 6833 m² (269 trees), and according to aerial-based mapping it was 6883 m² – about 1% higher (285 vectorized crowns – 6% more). When considering tree species separately, the most consistent results among two techniques were obtained for birch: total crown area was underestimated by aerial method by 4%, while the number of trees was overestimated by 4%. For spruce, the total area of crown projections estimated by aerial photography was 14% less than by ground-based measurements, whereas the number of trees was 13% higher. According to the results of aerial photography, the crown projection area for oak was underestimated by 31%, and the number of trees was less by 13%. The results for aspen and lime showed high discrepancy between techniques, namely 1.5-2-fold overestimation of both crown projection area and number of trees for aspen by aerial photography, and 3-fold underestimation of these parameters for lime. The discrepancy in results obtained

by two techniques can be explained by accounting at aerial photography of smaller ($DBH < 5$ cm) trees in gaps, which during ground survey were omitted. One more reason can be due to the uncertainty of recognition of similarly looking aspen, birch and lime on aerial photo. The underestimation of crown projection area with aerial photography could be actually the overestimation of this parameter by ground survey resulted from too rough approximation of crown projection shape. In addition, the parts of single trees' crown, branched at small height above the ground, could be recognized on orthophotomaps as individuals crowns. The work was supported by Russian Science Foundation (project № 18-14-00362).

Hedysarum zundukii Peschkova (Fabaceae) mapping – the Russian Red Book species

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The purpose of this work was to obtain current data on the *Hedysarum zundukii* spreading, the species which is protected at federal and regional levels. This is a narrow-endemic of the Baikal western coast. The species is considered to be a relic of ancient preglacial desert-steppe flora. Its distribution area is limited to the Olkhon district of Irkutsk oblast on the territory of the Pribaikalsky National Park. Before mapping, there were only 50 register entries introduced to the Phytodiversity Database of Baikal Siberia (19 records were doublets). Specimens are stored in the herbarium collections of the Komarov Botanical Institute of the RAS, St. Petersburg; Tomsk State University, Tomsk; Central Siberian Botanic Garden of the SB RAS, Novosibirsk; Siberian Institute of Plant Physiology and Biochemistry of the SB RAS, Irkutsk State University, Irkutsk. In July 2018, we tried to establish the boundaries of the range clusters of the *H. zundukii* using GPS, and also to mark the individual specimens, growing outside clusters. The total number of the GPS-points obtained in field-studies is 265. Each point corresponds to a specimen, growing on the boundary clusters, or to a single specimen, growing outside clusters. According to our data, the distance between the extreme points is 19.3 km. The boundaries

of the area are located within 53°20" and 53°28" north latitude, 107°16" and 107°30" east longitude. Despite the fact Oto-Khushun Cape is marked on a wide range of labels as the specimen's location, our data show that the southernmost location of this species is situated 2.5 km to the north of the tip of the cape of Oto-Khushun (IRK). Probably, the old specimens with Cape Oto-Khushun marked as location were collected more to the north of the cape, since there are no suitable habitats for this species on the cape. The northernmost location is Cape Zama. The easternmost point coincides with the northernmost one, and the westernmost point coincides with the southernmost one. There are 5 main clusters ($S = 53685.9 \text{ m}^2$). 1) $S = 450.22 \text{ m}^2$, the northeastern part of Khuzhir Cape. 2) $S = 27115.35 \text{ m}^2$, length 500 m, average width 100 m, 450 m to the northeast of the first cluster, between the capes of Khuzhir (1.5 km to the north-east) and Khargantui (Hohe-Nahoytuy) (3 km to the south-west). 3) $S = 1096.40 \text{ m}^2$, length 200 m, 2.6 km to the north-east of the second one, in the western part of Cape Khargantui (Hohe-Nahoytuy), on the coast of the Gulf of Kargante. 4) $S = 20328.56 \text{ m}^2$, length 540 m, 1.6 km to the northeast from the third, in the western part of Cape Zunduk in 800 m from its tip, right bank of the Zunduk river, 1 km to the west from the estuary. 5) $S = 4695.37 \text{ m}^2$, length 200 m, 1.5 km to the north-east from the fourth, in the eastern part of Cape Zunduk, left bank of the Zunduk river, 800 m from the estuary. This study was supported by the Russian Science Foundation (grant 16-16-00080).

Higher plant cadaster of the Kemerovo region

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Кадастр высших растений Кемеровской области

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The most important trend in development of modern botanical research and improvement of the educational process is widening of tasking for information processing and storage with the involvement of the latest advances in botany, phytocenology and phytogeography. At the premises of the Institute of Biology, Ecology and Natural Resources at the Kemerovo State University we have developed the “Higher plant cadaster of the Kemerovo region” database (Certificate № 2017621117) and the database application (Certificate № 2017660731). The database includes a class list of higher plants of the Kemerovo region (over 1600 species). The product advantages are ease of operation, feasibility of using standard configuration computers. The application allows working on IBM-PC compatible computers, with the operating system version Windows XP and higher. It is produced by the “C++ Builder” environment with network support (Firebird). The application performs runtime multi-parameter information sampling and the floristic analysis for a selected list of plants. Several users can work with different lists simultaneously. We have implemented 10 basic modules with over 500 characteristics. The Taxonomic position module includes the Russian and Latin names of the plant division, family, genus, species, and synonyms. It allows searching by taxons. The Biomorphe module contains information on the lifetime and fructification, phenorhythmotypes, life-forms. The Morphology module contains data on morphological traits of flowers, inflorescences (the flower marking, gender and symmetry, perianth, gynaecium, inflorescence types) and fruits. The Biology module includes modes of pollination, fruit dispersal, times of flowering and fruiting (sporulation). The Ecogroup module displays the species behaviour to ecological factors (water, light, soil fertility and acidity, its texture and mineral composition). The Geography module contains data on the species endemism, relictiness, area type, and its altitudinal, zonal, meridional distribution; for adventitious species – on their advent modes and time, rate of introduction, infective status. The Resource significance module identifies the species economic value and range of application. The Habitats module indicates the species distribution in various phytocoenoses and phytogeographical zones. The Protection module defines the species belonging to wild kins of cultivated plants, its conservation status (federal, regional) and category of rareness. The Species description module is related to literature sources. The cadaster is used in scientific research, for preparation of publications (graduate qualification works, articles, conference proceedings, regional Red Books, reports), and in the educational process for teaching biological disciplines of the

bachelor's degree, master's degree, research degree levels. Basing on the cadaster we are currently working on development of the "Herbarium of the Kemerovo region (KEM)" database.

Hordeum jubatum L. dataset of occurrences

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We used an information-analytical system on the Baikal Siberia phytodiversity (Verkhozina et al., 2016) in our attempt to collect most complete information on *Hordeum jubatum* L. distribution. The species is quite widespread in most parts of Eurasia, but is considered to be native only in the western and northern regions of North America (Bothmer et al., 2007). In most Siberian regions, the species is regarded as invasive, and even as a "transformer" in the Altai Territory, the Republic of Khakassia, and in the Irkutsk region (Black Book ..., 2016). Currently, this database has 1014 georeference records, including data on collection date, location and habitat, collector, and herbarium collection where the specimen is stored. Specimens from the herbarium of the SIPPB SB RAS (IRK) collected from 1982 to 2018 from the Baikal Siberia and Sakha Republic were also taken into account. Data from other herbarium collections (ALTB, HGU, IRK, IRKU, KEM, KRAS, KUZ, LE, MAG, NS, NSK, OMSK, TK, UAM, UBC, UUH, VLA) in amount of 917 records from 36 subjects of the Russian Federation (Region: Arkhangelsk, Chelyabinsk, Irkutsk, Kemerovo, Kostroma, Kurgan, Leningrad, Magadan, Moscow, Murmansk, Novosibirsk, Omsk, Ryazan, Saratov, Tomsk, Tver, Tyumen, Vladimir, Yaroslavl; Republic: Altai, Buryatia, Chuvash, Khakassia, Sakha, Tatarstan, Tuva, Udmurt; Territory: Altai, Kamchatka, Khabarovsk, Krasnodar, Krasnoyarsk, Primorsky, Trans-Baikal; Chukotka Autonomous Region; Khanty-Mansi Autonomous Area) and 6 foreign states (Canada, Kazakhstan, Mexico, Turkmenistan, Ukraine, USA) from 1818 to 2018 were also added to the database. Collect-

ing information on species distribution is still an ongoing process. Subsequently, it is planned to provide data in accordance with the Darwin Core standard, and to publish it in the GBIF (<https://www.gbif.org>) via the Integrated Publishing Toolkit (IPT). This will not only help with monitoring this invasive species and preventing its spread based on modeling of its distribution area, but it will also make the data stored in local herbarium databases available to the global scientific community. This work was supported by RFBR grant 16-04-01246 and RFBR and Government of Irkutsk oblast grant 17-44-388084.

How much data do Russian biological collections contain?

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Сколько данных хранится в российских биологических коллекциях?

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Best known and largest Russian herbarium collections are stored in Komarov Botanical Institute (LE, more than 6 mln sheets) and Moscow University (MW, more than 1 mln sheets). The largest zoological collection is located in Zoological institute and counts more than 60 mln specimens. There are also many different another biological collections in Russia, but unified list about them is absent and related information is scattered. There are 81 biocollections from Russia registered on the Global Registry of Biodiversity Repositories (<http://grbio.org>). According to the portal Genetic and biological (zoological and botanical) collections of the Russian Federation (<http://www.sevin.ru/collections/>), 145 herbarium collections from 102 cities were present in Russia in 2004. During this work

we founded information about 160 regional herbarium collections with total storage more than 8 mln specimens (excluding MW and LE). There are also 4 Russian live algae collection, total storage are 1258 living specimens (<http://www.wfcc.info/>). Available data on zoological collections are poorer. Large collections are stored in the Zoological Museum of Moscow University (6378700 specimens), the Museum of Institute of Plant and Animal Ecology (1150023 sp.), the Institute of Biology of Komi (118576 sp.) and the Museum of National Scientific Center of Marine Biology (about 1 mln sp.). The majority of Russian biological collections are not digitized. In our assessment total amount of digitized samples is about 1 mln, mostly presented by MW herbarium (99.5%). This collection almost completely digitized and now available through GBIF.org (doi 10.15468/cpn-hcc) and thematic information system (<https://plant.depo.msu.ru/>). A small part of the LE and SVER herbaria are also digitized (1320 and 5031 sp. respectively). Generalized data of labels for herbarium collections of the Polar-Alpine Botanical Garden-Institute of N.A. Avrorin KPABG, N.I. Vavilov Institute of Plant Genetic Resources (VIR) and the Prioksko-Terrasnyi Biosphere Reserve also available via GBIF.org (total 39114 records; doi 10.15468/yxt7co, 10.15468/nctfm2, 10.15468/80tu83, 10.15468/xtcciv, 10.15468/cjzloe, 10.15468/r8ybnq). Thus, at least 82 million specimens are stored in Russian biological collections, but available (via the Internet) data is only 1.2%. This work is partly supported by a GBIF - FinBIF data mobilization grant for European Russia (project Russia-02).

Informational and analytical support of floristic diversity researches in the Middle Volga region – SALIX system

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Информационно-аналитическое обеспечение исследований флористического разнообразия Среднего Поволжья – система SALIX

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With the aim of integrating, storing, processing and using data on the floristic diversity of the Middle Volga region, the Salix Information System (State Registration Certificate No. 2017660489 of September 22, 2017) has been developed at the Institute of Ecology of the Volga Basin of the Russian Academy of Sciences. The Salix system allows adding and viewing the information about plant taxa, using the extensive filtering and sorting options for taxonomic and environmental criteria, recording plant detection points georeferenced to geographical coordinates, administrative and floristic areas, view detection points using the Yandex.Map interface, managing the links on literary sources concerning the points of plants and individual taxa detection. The system provides for the possibility of a single entry of an array of species-specific floristic information for a particular point, while simultaneously matching the taxa available in the database, as well as the possibility of introducing new taxa and new administrative areas. The Web application is built on the current ASP.NET MVC 6 Web technology in the Visual Studio 2013 Express development environment; MS SQL Server Express 2016 is used for data storage. The application is deployed on a server running Windows Server 2012 R2; IIS 8 serves as the Web server. Data entry and editing, including spatial data, can be performed from any computer connected to the Internet. In the system, it is possible to upload the filtered data to an Excel file for later analysis. Thus, the Salix information-analytical system allows quick provision of data on floristic diversity within a large region, timely recording of the floristic findings, taking into account the latest nomenclature changes, visualization of floral information, identification of plant species peculiar to the area, localities of rare plants, and places of concentration of alien species including invasive plants.

Information and analytical aspects of *Linum usitatissimum* L. cultivation: biodiversity and directions of use in Russia

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Content analysis of State Register of Selection Achievements showed that Register contains data on 37 varieties of oily flax, which are allowed for use in 8 regions of Russian Federation (Volga-Vyatka, Central Black Earth, North Caucasus, Middle Volga, Lower Volga, Ural, West Siberian, East Siberian). 25 selection achievements are patented, 8 varieties are created by foreign breeders (3 of them – by Belarusian, 3 – by German, 1 – by English, 1 – by Dutch). Russian breeders created 7 varieties in FSBSI ARRI of Oil Crops by V.S. Pustovoit (Krasnodar), 5 varieties in Russian Research and Design Institute of Sorghum and Maize “Rossorgo” (Saratov), 5 varieties in FSBSI Siberian Experimental Station of All-Russia Research Institute of Oil Crops by V.S. Pustovoit (Omsk region), 2 varieties in FSBSI Don Experimental Station by L.A. Zhdanov of All-Russia Research Institute of Oil Crops by V.S. Pustovoit (Rostov region). During the last 5 years, 23 selection achievements are included in State Register. Four new varieties were included in 2018, three of them (Ilim, Salyut and Focus) were created in Belarus (RSSUE Institute of Flax), originator of fourth variety – Yalta is OOO “ASK” (Stavropol). Salyut variety is allowed for use in Volga-Vyatka, Lower Volga and West Siberian regions. Ilim variety – in Volga-Vyatka and West Siberian regions. Focus variety – in North Caucasus and Lower Volga regions. Yalta variety – in North Caucasus region. Traditionally, mostly morphological description and economical features are given in characteristics of introduced and selected forms of intermediate and crown flax (crop yield, mass of 1000 seeds, vegetation period, fall and drought resistance, disease resistance). Only one biochemical parameter – fat content – is generally given. In our opinion, this is not enough. Research of fatty acid and amino acid composition showed that qualitative and quantitative phytochemical parameters of oily raw material can be used as chemotaxonomic criteria of intraspecific forms. For example, content of essential polyunsaturated fatty acids and essential amino acids can be used. Such parameters can determine technical, nutri-

tive and pharmacological value of flax seeds and products of its primary processing. Also, directions of use of flax seeds can be determined on the base of these parameters.

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biochemical parameter – fat content – is generally given. In our opinion, this is not enough. Research of fatty acid and amino acid composition showed that qualitative and quantitative phytochemical parameters of oily raw material can be used as chemotaxonomic criteria of intraspecific forms. For example, content of essential polyunsaturated fatty acids and essential amino acids can be used. Such parameters can determine technical, nutritive and pharmacological value of flax seeds and products of its primary processing. Also, directions of use of flax seeds can be determined on the base of these parameters.

Introducing a sequence database management system (SeqDB) at the Swedish Museum of Natural History and how to export to external systems

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Natural history collections contain valuable resources, such as type specimen for authoritative identification using approaches that include phenotyping, DNA barcoding, and whole genome sequencing. The rapid development in DNA technology has increased the need for an efficient and well-integrated infrastructure for DNA barcoding, including automated work flows for both a digital and physical DNA archive. This presentation will give an overview and significant details of the structure, and the current status of the SeqDB system developed by Agriculture and Agri-Food Canada (AAFC) and its customized implementation for the Centre for Genetic Identification and the DNA-lab at the Swedish Museum of Natural History (SMNH). SeqDB tracks the complete workflow and provenance chain from source specimen information through DNA extractions, PCR reactions to sequence and/or genotype data. Thus, having the functionality as a Laboratory Information Management System (LIMS) to enable traceability. SeqDB implements

the Taxonomic Databases Working Group (TDWG) Darwin Core (DwC) standard for Biodiversity Occurrence Data, as well as the Genome Standards Consortium (GSC) ‘Minimum Information about any (x) Sequences’ (MIxS) specification. Furthermore, SeqDB tracks sampling metadata and DNA extractions from Next Generation Sequencing (NGS) of environmental samples and tracks the physical samples stored in racks of pre-printed vials. All the information is presented using a graphical user interface that features intuitive molecular workflows as well as a RESTful API that facilitates integration with external applications and programmatic access of the data. SeqDB currently support exports to GenBank and BOLD (Barcode of Life Data Systems) and will in the future also support exports in the GGBN DwC standards. Besides the already available functionality, the SMNH instance of SeqDB has been extensively evaluated to handle large-scale genotyping, as part of the Swedish Environmental Protection Agency monitoring programs. These data are publicly accessible and can be searched using a public-UI. The long-term goal is to couple the SMNH SeqDB instance with external APIs such as Rovbase (a database hosting wildlife observations in Scandinavia). SeqDB will provide significantly better opportunities for SMNH to rationally handle large amounts of samples, thus enabling larger projects to be carried out based on DNA analyzes, not least DNA barcoding projects.

Large-scale aerospace photography, soil-geobotanic profiling in the geobotanical mapping (discover aspects of the phytocoenotic and biogeocoenotic diversity)

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Крупномасштабные аэрокосмические снимки, почвенно-геоботаническое профилирование в геоботаническом картографировании (аспекты

выявления фитоценотического и биогеоценотического разнообразия)

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The study is based on using the method of large-scale mapping of the vegetation in conjunction with field aerospace photography interpretation of a different scale by generating maps on a scale in 1 : 10 000 – 1 : 100 000. By laying transect-profiles and using geobotanical descriptions for different years, it is possible to identify areas reflecting the whole spectrum of the typological diversity and composition of the region's communities. These model areas are representative throughout the entire different spatial structure and diversity of vegetation communities, biogeocoenotic diversity and are the objects of monitoring of the dynamics and genesis of communities that develop in different environmental conditions and reflecting different plant communities of the region's vegetation. The aim of this study is determining of main peculiarities of structure and dynamical plant communities organization forming under the conditions of mutual development different types of vegetation for concrete territory. A many-year monitoring in the model areas using aerospace photographs from different years for the territory of the different region is instrumental in revealing the typological composition of communities with a central set of plant species, diagnostic tools for communities of different conditions of development. The selection of a territory where profiling is to be performed requires always natural phenomenon analysis, its concrete characteristics or a particular structure and is always individual. The relief structure, taking into account differences in relative heights, the situation of a territory in a mountain system, if available, as well as triangle system analysis (river basin, lake coast, etc.) determine the profile site and length. A geobotanic profile aimed to reveal the spatial variability of communities structure is established taking into account the peculiarities of vegetation communities on the a territory depending on the range – topological, regional, zonal, etc. One of the methods for revealing structure, spatial variability and interaction of phytocoenosis in different environments conditions with edaphic conditions, on our opinion, can be combined soil-geobotanic profiling. Due to the application with material of perennial monitoring and geobotanic

survey on the base of aerospace photography, soil-geobotanic profiling favored the resolution of such tasks as establishing of phytocoenotic diversity, the structure of communities forming in the different environmental conditions concrete territory. Using methods combination of geobotanic survey with large-scale mapping of vegetation on the base of field deciphering of aerospace photography together with phytocoenosis monitoring during different seasons and years allow to get the dates about biogeocoenotic diversity as well.

Living Atlases Community

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Since 2010, the Atlas of Living Australia (ALA) provides information on all the known species in Australia and contributes to the Global Biodiversity Information Facility (GBIF). By lending access to this national open source platform, the open and modular architecture of ALA enables re-use of ALA tools by other countries and regions. Over the years, thanks to the ALA team and GBIF, the community has grown in different ways from production to training courses. Firstly, data portals based on ALA but residing outside Australia, have been launched in several institutions such as INBio in Costa Rica and Canadensys in Canada, and in the GBIF network via at least eight nodes presently operating national ALA-based portals (e.g., Spain, Portugal, France, Sweden, Argentina, United Kingdom). Others will follow in the coming years (e.g., Colombia, Peru). Other countries, such as Benin, have also begun to develop their own installations with the aid of partners in the Living Atlases Community. Secondly the experience gained by installing and customizing their own data portals has allowed many advanced participants to share their expertise in subjects like internationalization, data management, and customization, with others during workshops. Adding to these points, as an open source software, developers contribute to the community by implementing new functionalities and improving the translation into several languages for users of the software. Today, some modules are fully translated into Spanish, French,

and Portuguese. One of the main objectives of this presentation will be to present the community of Living Atlases by showing examples already in production (Atlas of Living Australia, Canadensys, GBIF Benin, GBIF Spain or NBN Atlas), past & future projects involving the community and highlighting how re-using existing software can be motivating and stimulating.

Mapping Asia Plants: Initiative and Progress

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Mapping Asia Plants: Initiative and Progress Keping Ma^{1,2}, Xuehong Xu^{1,2}, Maofang Luo^{1,2}, Bo Liu¹, Hongfeng Wang¹, Jianhua Xue¹, Qinwen Lin¹, Wenjun Li³, Zheping Xu⁴, K. N. Ganeshaiah⁵ 1 Institute of Botany, Chinese Academy of Sciences, China 2 Biodiversity Committee, Chinese Academy of Sciences, China 3 Xinjiang Institute of Ecology and Geography, Chinese Academy of Sciences, China 4 National Science Library, Chinese Academy of Sciences, China 5 University of Agricultural Sciences, GKVK Bangalore, India Because of the huge population and rapid growth of economy, biodiversity including plants are being seriously threatened in Asia. Researches on conservation and sustainable use of biodiversity are depended on species cataloging and monitoring to a great extent. But till now, there is no biodiversity database infrastructure in regional scale in Asia, while there are certain independent efforts of Biodiversity database construction in China Mainland and China Taiwan, India, Japan and Korea, which has serious impacts on biodiversity research and protection at regional scale in Asia. Thus, Mapping Asia Plants (MAP) was initiated at the meeting of ABCDNet(ABCDNet, www.abcdn.org) working group on Nov., 2015, and was funded by Bureau of International Co-operation and Southeast Asia Biodiversity Research Institute Chinese Academy of Sciences. MAP provides a database and standardized workflow for mapping

Asia plant species, distribution, and is available to comprehensive basic information and interdisciplinary data mining for plant diversity conservation and research. MAP aims to collect, integrate Asia plant diversity resources and to construct a platform of Asia plant diversity. Major achievements so far are as follows. Species checklist databases have been basically set up in five sub-regions of Asia (Southeast Asia, South Asia, Northeast Asia, North Asia and Middle Asia) to the national level, and the species checklist databases have been basically set up in 3 countries in West Asia. 1) for Southeast Asia, a dataset of 425 families, 4873 genus, 69291 species has been set up; 2) for South Asia, a dataset of 325 families, 3817 genus, 32525 species has been set up; 3) for Middle Asia, a dataset of 169 families, 1404 genus, 9047 species has been set up; 4) for Northeast Asia, a dataset of 417 families, 4345 genus, 42566 species has been set up; 5) for North Asia, a dataset of 191 families, 1187 genus, 7700 species has been set up; 6) for West Asia, a dataset of 200 families, 2543 genus, 6000 species has been set up.

Modeling of areas of cladotype species of plants of the nemorose refugia of the Khamar-Daban ridge using the maximum entropy method

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Моделирование ареалов реликтовых видов растений неморального рефугиума хребта Хамар-Дабан методом максимальной энтропии

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Bioclimatic modeling allows not only mapping the areas of certain plant or animals species on the basis of environmental characteristics, but also to investigate the influence of environmental factors on the occurrence of these species. We simulated the potential areas of the three groups of species of higher vascular plants on the northern macroslope of the Khamar-Daban ridge. For modeling we selected species whose distribution in Baikal Siberia is completely or predominantly restricted by the Khamar-Daban ridge, which are nemorose cladotypes and included in the Red Lists of various rank. The first group is the most numerous and includes species distributed only in the lower reaches of the river valleys and along the foothills of the slopes. In the altitude relation they occur from 456 m (Lake Baikal level) to 700 m. The species of the second group occur almost exclusively in the subalpine and alpine belts, starting from an altitude of 900 m. The species of third group are widely distributed both in the forest and subalpine belts from Baikal to 1600 m. As a parameters of the environment we use the relief characteristics calculated on the basis of the digital elevation model SRTM, as well as the parameters computed from the three differently seasoned cloudless satellite images Landsat 8 (all with a resolution of 30 m) with the use of tasseled cap algorithm as well as NDVI. Using the MaxEnt software models of potential range for each group of species is created. It is revealed that the main factor of the environment influencing the occurrence of the species under study is altitude, and secondary factors are the vertical distance to channel network and various Tasseled cap parameters. The distinction of potential areas of all three model species groups reflects their different ecological requirements. The results of the simulation confirmed the conclusions obtained on the basis of expert analysis of the investigated refugia and the confinement of species to certain locations, but allowed us to delineate the areas of these refugia, which is difficult to do only on the basis of data on the locations of species. In the future, it is planned to use the data obtained to more accurately determine the boundaries of the refugia of nemorose plant species and to identify environmental factors that affect their formation. The work performed reveals patterns of spatial distribution of biota, which are used to solve problems of conservation of biological diversity. The work was carried out within the framework of the program of the V. B. Sochava Institute of Geography SB RAS № 0347-2016-004 and № 0347-2016-003 with partial support of the Russian Foundation for Basic Research (projects № 16-05-00783).

Model mapping of phytoplankton biomass from remote sensing data

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Модельное картографирование биомассы фитопланктона по данным дистанционного зондирования

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As known phytoplankton is the lowest level of the trophic chain determining the aquatic ecosystem productivity. It is possible to obtain the information about the surface phytoplankton distribution over a large area by the modern remote methods. The satellite signal penetrates only into the upper layer, so these methods are limited. In fact, the plant biomass volume located under the surface water layer may differ significantly from the remote data. To reconstruct the integral biomass in the whole water column under a unit area, a vertical model of phytoplankton functioning based on the concept of fitness function is used. The phytoplankton community is considered under its aspiration to occupy the niche most favorable for life. In this case, the community growth rate coincides with the specific growth rate of phytoplankton. The model solution reduces to solving the Cauchy problem for a system of ordinary differential equations with the remote sensing data as initial conditions. The specific phytoplankton growth rate is a multiplicative dependence on the main external environment parameters such as mineral nutrition, temperature, irradiation and others. The remote sensing data of the Sea of Japan and Issyk-Kul Lake are used for the model testing. A verification method depends on the data available to the researcher in addition to satellite information. We used literature data, a biogeographical description of the Sea of Japan, as well as data obtained in vivo on Issyk-Kul Lake. The geographic object is represented by arrays of the surface values of the chlorophyll concentration, temperature and irradiation in each node of a uniform grid, if it

is free from cloudiness. To solve the vertical model, the depth maps were digitized in order to determine the limiting aquifer at each point of the object subjected to satellite processing. Biomass values in the areas covered by clouds are obtained by automatic triangulation using support nodes in which the numerical solution data are correct. The model solution visualization gives an idea of the spatial distribution of biomass within the entire zone where the photosynthesis takes place.

Moscow Digital Herbarium: OCR-mining of the text data for the Russia's largest biodiversity database

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Цифровой гербарий МГУ: добыча текстовых данных с помощью OCR для крупнейшей в России базы данных по биоразнообразию

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Moscow Digital Herbarium (<https://plant.depo.msu.ru/>) is the sixth largest library of imaged herbarium specimens in the world. We are adding constantly new images of recently collected specimens, transcriptions of the labels, and manual georeferences. As of 4 May 2018, Moscow Digital Herbarium hosts 911,543 images of 914,324 specimens, 101,415 captured labels, and 109,375 georeferences. It is fully indexed in GBIF delivering to a wider community ca. 75% of occurrences published by Russian institutions. A herbarium specimen with both a dry plant and a label mounted on a sheet of paper is a convenient object for 2D imaging and further OCR-mining of text data. Since March 2018, we implemented the OCR procedure for an automatic label capturing following best practices of New York, Paris, and Edinburgh herbaria (NY, P, E). After some tests we decided to use open-source Tesseract software. Rough results of the OCR were cleaned by ca. 50 sophisticated quality-checks and mistake

erasers. Finally, we left only "long" results with at least 100 characters and 5 words. We combined up to four languages in the OCR procedure, although English + Russian were used as a default combination. Labels with words characteristic for the German language were processed repeatedly in the German mode (ca. 2,000 labels of bryophytes). We used OCR transcriptions of labels for the following further activities. (1) Searching for the collections of definite collectors to link the images with existed tables from which labels were initially produced. (2) Searching for the collections with printed coordinates for quick georeferencing of these specimens. (3) Country-tagging of the extra-Russian collections for further processing of labels using country filter. (4) Region-tagging of the Russian collections for further processing of labels using regional filter. (5) Searching for the mistakes in manual attribution of a country or a herbarium area and label capturing implemented earlier. Thereby, we do not use the text data mined by the OCR instead thorough label capturing. We regard it as a powerful tool for pre-selection of specimens which makes the database management more efficient. MW digitisation was supported in 2015–2018 by the grant № 14-50-00029 from the Russian Science Foundation (RNF).

Multivariant approximation of observational data characterizing biodiversity and individual development at the organisms level

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Многовариантная аппроксимация данных наблюдений, характеризующих биоразнообразие и индивидуальное развитие на организменном уровне

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Revealing the types of elements considered as "semantic" units that determine biodiversity at the organisms level presupposes the definition of invariant for each type that can be matched to specific heredity. In the process of individual growth and development, different genotypes under the influence of environmental factors may have a similar dynamics of changes in one subset of phenotypic characteristics and various in other. The selection of subsets of characteristics is determined by the similarity of functional dependencies, often non-linear, connecting the characteristics in each subset. In fact, this assumes the need for solution of one and the same problem by mutually combination of cluster and regression analysis techniques traditionally used sequentially. It seems advisable to change the problematic setting that occurs when statistical analysis (for example, regression analysis) of morphometric data is performed, namely, to obtain as large as possible number of reliable non-duplicating formula dependencies linking the values of the characteristics determined as a result of specific study, instead of confirming or disproving the assumption of connections availability between a priori formed subsets of them. In addition, it is necessary to take into account the possibility of existence of dependencies, which include variables that are not present in the observational data, in particular, characterizing the changes in the values of the directly measured characteristics at certain intervals of time. Let's consider the main features of the proposed approach to data processing. An abstract scheme for presenting data (of observations) is cube which axes correspond to: objects, variables (characteristics), moments or time ranges. When using standard methods of statistical data processing, the cube is unfolded to object-attribute flat table with modifiable set of columns. Following problems are consistently solving in automated mode: 1. Replenishing of the axis of attributes with "computable" variables that are absent in the observations and using of changes in values of variables at certain intervals of time as additional attributes. 2. Identifying the relationships between variables included in the replenishment set and the formation of corresponding set of linear and nonlinear formulaic dependencies. 3. Selecting groups of objects (corresponding level) based on the similarity of functional dependencies. The report discusses two examples of methods described which are using for formation of the sets of formulaic regression dependencies characterizing the features of Scots pine morphogenesis: in stands with growth anomalies (significant deviations in growth processes from the norm) and in pine young growth in the temperature of environment gradient (in the zone of associated gas flare impact).

On the analysis of the spatial and interannual features of phenological stages of forest vegetation by the use of vegetation indices when the cloudless satellite images are limited

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Об анализе пространственных и разногодичных особенностей фенологического развития лесной растительности с использованием вегетационных индексов при ограниченном количестве безоблачных сцен

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Climate change heavily impacts on growing conditions and expanding coverage of arboreal species and forest communities (Vose et al, 2011; Xiao-Ying, Chun-Yu, Qing-Yu, 2013, and others). The analysis of the spatial and interannual features of phenological stages of forest vegetation by the use of various vegetation indices (NDVI and others) proves effective in forecast of such tendencies. The use of a logistic model is the most effective approach to the analysis of seasonal changes of vegetation indices (Melaas et al, 2013). The model allows to calculate the time of the beginning of the seasonal growing, the middle of the spring growing, the time of the

transition to the summer growing and the rate of the seasonal development for the period of spring development of tree stands by the inclinations of an ascending line of the diagram. A considerable amount of cloudless satellite images is devoted to determine the gearshift points of the seasonal development in the diagram. It is possible only for territories with an arid climate or, for example, if the medium-resolution images MODIS are used. When Landsat 7, 8 and Sentinel 2 images are used for the mountainous forest areas of Southern Urals Mountains there was lack of images suitable for analysis of the seasonal NDVI dynamics in a certain year. A reference diagram constructions method was therefore developed to determine the NDVI dependence on the stage of seasonal vegetation development; for this the interannual data were grouped together and then they were compare to NDVI for a certain year. The interannual satellite images of some plots of the Bashkir State Reserve were used to test the method; regular terrestrial phenological observations were conducted in these plots. The dates of the beginning of seasonal growing and the duration of phenological stages differed in different years; thus, the average annual dates of the beginning of various phenological stages and their durations were calculated. From this information, the time of beginning of the stages and their duration were normalized for the certain years. After that, the position of the images on the time axis shifted in a proportionate way. As a result, the interannual data with the same NDVI has moved to the same position in the axis of the phenological development. With the example of the birch woods of the mountainous forest areas of Southern Urals Mountains it was revealed that the reference diagrams enable analysis of deviations from the rate of the seasonal forest development depending on weather conditions in certain years; they also enable to study the features of the seasonal development of forests in areas differing in climatic conditions.

Peculiarities of dynamics of plant life forms of the meadow communities of the Ugra National Park at different conditions of anthropogenic impact revealed by using multi-year monitoring data

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Особенности динамики жизненных форм видов растений луговых сообществ национального парка “Угра” при разных условиях антропогенного воздействия на основе данных многолетнего мониторинга

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At present, there are significant changes in the floristic composition and functioning of various phytocenosis under the influence of anthropogenic factors. In this regard, a thorough and comprehensive study of these changes is needed, it is also necessary to make forecasts and recommendations for the rational use of plant communities. The modern development of information technologies allows an assessment of the changes occurring in plant communities quickly and effectively, to evaluate and simulate the development of natural processes, in particular, in the economic use of meadow communities. The aim of the work is to reveal the influence of various conditions of anthropogenic impact on the dynamics of the life forms of plant species in Zalidovo meadows using the Lifeform Index (LI) and the Life Stability Index (LSI). The results on using different indices to analyze the dynamics of the meadow community based on more than 50 years monitoring data for Zalidovo meadows (Kaluga Region) are presented in the report. As model objects, six trial plots were selected, which were under different conditions of anthropogenic impact in the period of 1961-2012. With the use of LSI it was shown that the greatest variety of life forms was achieved on the plot that was used for all years of monitoring as a hayfield, on which perennial life forms of meadow plants predominated. The smallest value of diversity was found in areas which were used mainly as pastures, dominated by annual and biennial life forms. The comparative analysis of the LSI for all plots based on the one-way factor analysis of variance (ANOVA) showed that there was not statistically significant difference between the studied plots, which indicated a high

level of the growing life form stability in the studied plots. The analysis of the dynamics of the meadows life forms makes it possible to assert that haymaking and pasture regime affect the growth of the life forms of meadow plants in different ways. Haymaking increases the participation of perennial life forms, and pasture regime increases the participation of biennial and annual life forms. The conclusion is: the most optimal use of meadows is the alternation of haymaking and pasture regime.

Phytomass production of vegetation near lake Baikal

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Накопление фитомассы растительностью на побережье озера Байкал

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Phytomass production is one of the important functions of landscapes. The amount of phytomass depends on regional (radiation balance, precipitation, and history of land-use development) and local environmental factors such as the structure of geosystems and their dynamical stage, the features of individual geosystem components – relief, soils, species composition of plants, etc. Natural landscapes surrounding Lake Baikal provide a lot of ecological functions including the phytomass production and other environment formation functions. The aim of this investigation is the assessment phytomass production and identifying the factors that affect this function using geosystem approach. We analyzed three study areas which are located in different parts of Lake Baikal (on the north-eastern shore – the piedmont of the Barguzin range; the western – the Priol'khonie; and southern shore – part of Khamar-Daban range). Study areas characterize the diversity of surrounding Lake Baikal's landscapes from steppes to boreal taiga. The landscape maps for these areas were compiled based on the analysis of fieldwork data, digital elevation

model, and remote sensing data. The stock of the tree stand phytomass and above-ground herbaceous phytomass was estimated in different landscape types based on fieldwork data (dendrometric measurements, grass cutting) and method of volume-conversion coefficients. In the result, the maps of phytomass stock for the study areas were compiled based on the method of landscape-interpretation mapping. Linear multiple regression analysis of the dependence of phytomass on environmental factors (aspect, height, steepness of slopes, degree of moistening, convergence index, annual amount of precipitation, sum of temperature higher than 10°C, thickness of humus horizon) at local and regional levels showed that the combinations of factors and the direction of their influence on phytomass production change depending on the local features of the landscapes. The research was supported by the Russian Foundation for Basic Research (№ 17-05-00588) and Russian Geographical Society (№ 2/2017 RGS-RFBR).

Pre-geoinformation-cartographic support for the development of new protected areas

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Предваряющее геоинформационно-картографическое сопровождение проектирования новых ООПТ

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Currently, GIS is used in many protected areas (PA), both for inventory, environmental monitoring, thematic mapping, and to assess the current state of the territory, functional zoning and management. GIS and mapping are of particular importance in the design of new PA. With the help of GIS, it is possible to perform multi-user tasks, such as the placement of infrastructure, regulation of livestock grazing, planning environmental protection measures and the choice of solutions that provide a minimum level of impact on

nature, conservation at the required level of biodiversity and protection of water bodies, especially in PA visited by tourists. On the scientific and methodological side in the design of PA important validity of geographic information and cartographic model, the suitability of its basic and applied potential to address the issues of conceptual support and management of PA. In the Altai Krai in the coming years it is planned to create several tourist-oriented PA - two national parks: "Mountain Kolyvan" and "Togul". There is an experience of creation of GIS at the design stage of the natural Park "Foothills of Altai" in the vicinity of the resort of Belokurikha. Pre-GIS of the Park solved various problems: - collection, classification and ordering of information on the design conditions of the PA; - data collection for the study of the dynamics of changes in the state of ecosystems and landscapes; - construction of thematic maps based on research results; - assessment of the situation and collection of additional (redundant) information to predict the development of the environmental situation on PA. With the help of GIS, the functional zoning of the natural Park was carried out, a preliminary aesthetic assessment was carried out for the placement of viewing platforms, tourist routes were laid and a protected protection zone was allocated. The territory of planned national Park "Mountain Kolyvan" pre-GIS was developed in 2002-2004 was created a database of field information to the project rationale of creation originally of the nature Park. The ecological and geographical analysis and mapping of the territory was carried out. Now borders of the planned national Park "Mountain Kolyvan" are changed, the area of PA is increased. The new version of GIS on the territory of the Park, created during the design phase, will update the existing data, integrate the new information received, as well as conduct monitoring studies using previously obtained data and maps. Work has begun on the creation of GIS national Park "Togul". Data are being collected and maps are being prepared. Application of geographic information methods and creation of GIS at the stage of PA design provides pre-project research, collection, systematization, storage of information, creation of a pilot prototype of GIS, as well as will contribute to a more complete analysis of the prerequisites and conditions for the creation of PA.

Regional information and analytical system on insect biodiversity of the Baikal region

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Региональная информационно-аналитическая система по биоразнообразию насекомых Байкальского региона

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The problem of biodiversity conservation is topical for modern ecology, because the scale of the impact of anthropogenic press on natural ecosystems is expanding at an accelerated pace. It is very important to study the spatial distribution of species. Insects play a huge role in the terrestrial ecosystems of the Baikal region. Therefore, the information and analytical system for assessing and monitoring of insect biodiversity in the Baikal region has been created. This system is consisting of three blocks: a) relational databases, b) the geoinformation system, c) the software environment R. Relational databases are designed to quickly find the necessary information and to automate the collection and structuring of data. Besides, these databases were created to analyze the requested information and to create an information basis for geoinformation system. In the structural and semantic respect, the databases consist of several parts: taxonomic, ecological, geographic. The geoinformation system was created to study the spatial distribution of insects. It covers the territory of three subjects of the Russian Federation (Irkutsk oblast, Republic of Buryatia and Zabaykalsky krai). All cartographic information in the geoinformation system is organized in the form of vector and raster layers: base (topological) layers, including rivers, roads, buildings, etc.; thematic layers (for example, entomological and landscape). Raster layers (cosmic images and digitized paper maps) were used when creating base vector layers. Moreover, due to the development of cartographic services on the Internet (access to high-resolution cosmic images, about 1 meter per pixel), vector layers with a wide scale range were created, which makes it possible to create both small-scale and large-scale thematic maps. This allows to study biodiversity at different levels. R is one of the most popular platforms for statistical computing and graphics, because it is free, open-source

software, with versions for Windows, Mac OS X, and Linux operating systems. Besides, additional modules (“add-on packages”) are available for a variety of specific purposes. At the present time, the features of spatial distribution of ants and buprestids have been explored by means of this information and analytical system.

Remote sensing techniques for investigation of grassland communities” diversity in the North-West of Russia

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Introduction and Question The object of our research is the diversity and spatial structure of herbaceous vegetation (meadows and semi-ruderal herblands) on the surrounding area of Polistovsky Reserve. We’ve developed the vegetation classification and attempted to model the distribution of communities using GIS and remote sensing (RS) technologies. GIS and RS technologies open a vast perspective for plant community researches. Remote data allow to map the communities and reflect their features (terrain, photosynthetic activity, productivity and biomass, etc). So understanding the place of each certain community within the dimensions of remote sensed data help us to get ecological “portrait” of them. The technology was effectively used for forests, but almost not tried for grassland communities, because 1) the spatial resolution of regularly available satellite images was not enough for grassland communities till 2016, and 2) along with the vision and infrared data, terrain is also critically important for community distinguishing - but the resolution of available digital elevation model is also not enough for grassland. Nowadays the improvement of data and techniques availability probably opens the new era for using RS for grassland researches. We use new available data (Sentinel-2 satellite images) and plan to include drone’s data for understanding spatial distribution of grassland communities. **Methods** We used the data of 205 grassland relevés (the point was marked by GPS) from

the surroundings of Polistovsky state natural reserve, Pskov region, Russia. The syntaxonomy of grassland communities was developed with Juice 7.0 . As RS data we used Sentinel-2 images and drones data which have been got while the field research and processed with Pix4D.com. Using ArcGIS 10.5.1, we extracted the remote sensing data (the normalized Sentinel pixel values, Kawth-Thomas and NDVI indices values), then using R 3.4.4 (Mann-Whitney test) analysed the distinguishing between syntaxa of some syntaxonomic ranks (from classes to associations). Position of the communities within Sentinel and drone data dimensions was also analysed with discriminate function analysis and Random Forest predictive algorithm. Results and Conclusion The diversity of herbaceous vegetation identified as 14 associations, 7 variants and 1 facie from 4 classes: *Molinio-Arrhenatheretea*, *Phragmito-Magnocaricetea*, *Epilobietea angustifolii*, *Artemisietea vulgaris*. The discriminate function analysis shows some uniqueness of classes in the dimensions of Sentinel-2 bands and vegetation indices. But the optical data is not enough for accurate distinguishing and modelling the spatial distribution of communities. We're waiting for crucial improvement of our result using drone terrain data and hope to share result and technology details by conference report. The reported study was funded by RFBR according to the research project № 18-34-00786.

Seed Bank as an essential part of the modern herbarium

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Extreme weather conditions, ongoing deforestation and extensive agriculture cause the irreversible loss of biodiversity, especially habitats for many plants, as well as facilitate the spread of invasive species, not only in the Tropical regions, but also in our neighbourhood. Species that were quite common just fifty years ago, are now endangered to extinction. By decades, herbaria were considered as a source of the information about biodiversity, but the dried specimens are nothing more than the silent witnesses of aggressive economy of the modern world. It is not possible to

restore wild population from the DNA inside the preserved tissues of the herbarium specimens. Though, the relatively inexpensive method – seed banking – allows to do it in an easy way. Seed bank does not only store seeds as an evidence of species occurrence, but also gives an opportunity for farmers and researchers to find varieties that could grow in different regions. And if the seeds are collected along the herbarium specimens, utility of the herbarium increases dramatically. Seed banks and herbaria are considered as an effective and complementary methods of preserving the biodiversity for further generations. There are about 1400 seed banks around the world, Svalbard Global Seed Vault being the most known, functioning as a global repository and a backup for other seed banks. However, smaller seed banks are not less important and value, but creating the herbarium related bank may be sensitive for miscarriage. Gathering of the seeds from the wild populations and further storage conditions for them, as well as merging and unification of data inside the database, are critical processes but strongly vulnerable for mistakes. Here we would like to discuss the problem and critical checkpoints for newly established seed bank, on the basis of the experience of creating Seed Bank collection funded along the Herbarium UGDA within the project “Protection of genetic resources of wild growing endangered species of vascular plants of Gdansk Pomerania”.

Study phytogeographical boundaries in Amur basin using species distribution modeling

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Исследование ботанико-географических рубежей в бассейне р. Амур с использованием моделирования пространственного распространения

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Russian part of the Amur River catchment area is the immense territory with diverse bioclimatic conditions. The aim of the study is to show main phytogeographical patterns of this area with using species distribution modeling (SDM) approach. SDM allows to determine response between species occurrences and environmental conditions as well as provide understanding of species distribution ranges with strong predictive capability. We selected 100 vascular plants species with diverse geographical distribution over the study area and a variety of zonal and altitudinal patterns. For the first time to East Siberia and the southern part of the Far East we form a dataset with 12371 georeferenced records and published it via GBIF: (<https://www.gbif.org/dataset/0c7bd9e3-ded7-4de4-99ec-d5145361ff48>). The dataset includes specimens of vascular plants deposited in seven major Russian herbaria: LE, MW, MHA, VLA, VBG, NSK, and TK. collected in the Amur Basin and adjacent seacoast in Russian Federation from 19th century. We georeferenced specimens manually using label localities. Based on this data we calculate species distribution models using MaxEnt. We choosed climatic (CHELSA bioclim and Global 1-km Cloud Cover variables) and remote sensing (MODIS land surface temperature, MODIS EVI) data as environmental predictors. Obtained models are adequately reflect the species ranges in the Amur river basin. We carried out an integral analysis of received models using clustering (Ward method). As a results we derived 11 clusters of species with similar distribution within study extent and estimated their climatic ranges. The identified groups of species indicate the distribution of the main vegetation communities types. Consequently we provided new phytogeographical data of vascular plants distribution in the Russian part of the Amur basin and mobilized herbarium specimens for further research.

Taxonomic and phytogeographical databases in systematics of the flowering plant family Umbelliferae/Apiaceae

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Таксономические и фитогеографические базы данных в систематике семейства *Umbelliferae*/Ariaceae (цветковые растения)

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Since the eighties of XX century several databases were compiled in the Botanical Garden of Moscow State University (MSU) in collaboration with the MSU Faculty of Computational Mathematics and Cybernetics and the MSU Computer Centre. These databases are connected with different aspects of critical investigations in systematics and geography of Umbelliferae, one of the largest and complicated plant families. The main goal is to incorporate, save and retrieve large data on scientific names, authors, synonyms, typification, characters, chromosome numbers, distribution and references related to genera and species of the Umbelliferae, and to accompany monographs, revisions and articles preparation in different aspects of the family systematics. Placing of the databases in Internet was out of our aims due to limited possibilities. The following databases were created – GNOM (Generic NOMenclator: on nomenclature, synonymy, and distribution of World Umbelliferae genera), CARUM (CARyologia UMbelliferarum: on chromosome numbers and karyotypes of World Umbelliferae species), ASIUM (ASIatic UMbelliferae: on systematics and geography of the genera and species of Asia), and the special descriptive single-purpose database on carpology of taxa, distributed in Eurasia and N Africa, being now in working out. The last one was elaborated since fruit characters are of essential value in the family systematics. These taxon-oriented databases reflect expert's opinions of the authors. The monographs "The genera of the Umbelliferae. A nomenclator" (based on GNOM; Pimenov & Leonov; Kew, 1993) and "The karyotaxonomic analysis on the Umbelliferae" (based on CARUM; Pimenov, Vasil'eva, Leonov & Daushkevich; Enfield, NH, 2002) were published. All four databases are widely used in current work, with a perspective of on-line publications. For the monograph "The Umbelliferae of Russia" (Pimenov & Ostroumova; Moscow, 2012) the multi-access key for taxa identification based on diagnostic character database was developed.

The Alien plants in the South Siberian flora database

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«The Alien plants in the South Siberian flora database» consists of interrelated tables, containing the following information: species distribution; species related publications for each species (separately for each region); way of introduction in the region; the time of the species appearance in the region; naturalization degree of the species in the region; way of diasporas' spreading; species amplitudes to the main ecological factors. Literature on new alien plants locations found out on the territory of Siberia in the last decades have been collected and analyzed to fill the database. Materials in the herbarium collections have been critically examined (Komarov Herbarium of the Botanical Institute, St. Petersburg; P.N. Krylov Herbarium of the Tomsk State University, Tomsk; Herbarium of the Central Siberian Botanic Garden of the SB RAS, Novosibirsk; Herbarium of the Kuzbass Botanic Garden, Kemerovo; Herbarium of the Siberian Institute of Plant Physiology and Biochemistry of the SB RAS, Irkutsk; Herbarium of the Irkutsk State University, etc.). By now, the database has information on 645 species of alien vascular plants spreading at least in one of 11 Siberian regions. For the each of this regions information on naturalization degree of alien plants has also been added to the database. The database structure has fields for references to scanned herbarium specimens and photographs of alien plant species in natural conditions as additional visual information. The work of linking references to the scanned herbarium specimens of alien plants, collected in Siberia, is underway. The work was based on the online accessible scanned samples from the Moscow Digital Herbarium, the “Noah”s Ark” project (<https://plant.depo.msu.ru/>). More than 200 references to the herbarium specimens have been added by now to the database. More than 250 references to photos of alien plants, which were made in Southern Siberia and placed in the on-line plant identifier “Plantarium”, (<http://www.plantarium.ru/>). Generally, the process of linking hyperlinks to publications, containing information on first findings of alien species in the Siberian regions, is completed. More than 600 of such references to publications, which are fully accessible online, are

included in the database, mainly these are articles placed in the Scientific Electronic Library (<https://elibrary.ru/defaultx.asp>). The herbarium labels data and georeferences of herbarium alien South Siberian samples are placed on the GeoPortal of ISDCT SB RAS (<http://biodiv.isc.irk.ru/#>). The database is available upon request, the species distribution maps are being formed automatically on the geoportal. This work was supported by RFBR grant 16-04-01246 and RFBR and Government of Irkutsk oblast grant 17-44-388084.

The Database of the Moss Flora of Russia

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The database of the Moss Flora of Russia were designed so to be maximally useful for the Moss Flora of Russia project, but aimed also for further accumulation of data on bryophyte distribution and potentially also on various aspects of their ecology and morphology. It currently includes over 138 000 herbarium labels from most Russian and some foreign herbaria. The database is made in the Firebird DMS for FreeBSD, and is kept in at least two servers in the Lebedev Institute of Physics and the Tsitsin Main Botanical Garden of the Russian Academy of Sciences. The common entrance to the database is from <http://arctoa.ru/Flora/basa.php>. The database includes information on the species localities, habitats and other standard label information. Data insertion/updating is processed by few authorized database managers through the form for uploading Excel (*.xls) files. On addition to queries, the database can 1) visualize species distribution upon yandex maps service; 2) comparison species compositions by selected regions; 3) show species diversity by grid squares in the areas defined by coordinates. Authorized users obtain additional possibilities, including building maps for several species of Russian moss flora. The data are continuously supplemented with a posteriori inserted geoposition data, and over 60% of labels now include such data. More information is given in publication at http://arctoa.ru/ru/Archive-ru/26_1/Arctoa26_001_010.pdf.

The experience of geo-referencing Central Siberia herbarium collections from the Moscow State University (MW) collection.

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Опыт географической привязки гербарных сборов Средней Сибири из коллекции Московского Государственного Университета (MW)

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The digitization of D.P. Syreischikov Moscow State University Herbarium (MW) has begun in 2016. The author, working in the Taymyr District of the Krasnoyarsk Region, set the goal of identifying all the collections of vascular plants from this region. Author's geo-referencing of collections (6300) was provided to MW to publish on portal also. During the work it became clear that for the full identification of the collection from Taimyr it is necessary to view the entire herbarium of region "Middle Siberia" (about 19500 samples). For the primary geo-referencing topographic maps 1 : 200000 used. Search locations of collection directly were conducted in the web mapping services (primarily Yandex. Maps). For collections of XIX - beginning of XX c. map the Yenisei Province from the Atlas of Asian Russia (1914) was used. If necessary, the reports of expeditions, publications of collectors and even biographical information about them were studied. After finding the desired area (by toponym), the transition into coordinates in the GIS ArcGIS project was carried out. The coordinates were specified according to the description of the place of collection and with the help of a special script were transferred to the MS Excel table with one click; collectors, collection date and expert accuracy of fixation in km were also entered there. After snapping the first 1000 examples areas of the main collectors determined, which allowed the ArcGIS project to set bookmarks on 36 areas. Now it is possible to perform up to 500 points per day. As shown, after such a "dip" in the collection of any example

can be mapped with an accuracy of from 0.5 to 5 km. In some cases, it would make sense to link not to the point with the radius of the error, but to a certain polygon or line feature (section of the river, the passage of the road, the vicinity of the settlement, etc.). The operator of the georeferencing should be well aware of the natural conditions of the region and have experience in field work. Thus, geographically localized areas of collecting, approximately corresponding to the concept of local flora, were determined. After the initial fixation of specimens, the opportunity for in-depth work in geographic samples appears. These samples will be used to clarify the bindings for satellite imagery, author descriptions of areas, as well as with the participation of current collectors. It is possible to name the first results of this work. Only within the Taimyr nearly 100 new locations of species have been identified, several species are new to the district. For the region it is possible to consider revealed some never published local floras – for example vicinities of the Igarka and Snezhnogorsk cities. The knowledge about the history of district flora study has greatly expanded. More than 100 sheets related to the wrong region were revealed. A significant number of knowingly incorrect or missing definitions are noted, which requires direct viewing in the Herbarium.

The ExStatR plugin for biodiversity research based on Excel and statistical package R

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Надстройка ExStatR для анализа биоразнообразия на основе Excel и статистического пакета R

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Today the free program for statistical analysis R became more and more popular (Seefeld, Linder, 2007; Kabacoff 2015). Now R is a “de facto” standard in most foreign and advanced Russian scientific schools

and science fields. R is a freely available language and environment for statistical computing and graphics which provides a wide variety of statistical and graphical techniques (<https://cran.r-project.org>). The biggest difficulty in using the R program is stems from necessity to create special scripts (small programs) that implement the necessary functionality. This prevents the wide expansion of the program R, especially in the natural sciences. We developed the ExStatR software module (Novakovskiy, 2016) that combines the Microsoft Excel spreadsheet and the R software environment. Using standard Excel spreadsheets as a data source makes it easy to enter, store and modify data. The software environment R is used as a computing core. This allows us easy add new or modify existing algorithms of data analysis, adjust the output parameters of table or graphic results. The implemented algorithms for data analysis are universal. This allows using the ExStatR module in many fields of ecology and biology. The module has a simple user interface and does not require special training to use it. To date, the following algorithms of data analysis are designed in module: ordination (principal component analysis – PCA, Non-metric multidimensional scaling – NMS), cluster analysis (UPGMA, Ward method, single-linkage and complete-linkage) and heat maps. Also it is possible to coloring objects and add correlation vectors of environmental factors. The developed scheme of interaction between Excel and R is modular. This allows designing new algorithms for data analysis and visualization of results fast and easy. The program is freely distributed. The installation version and detailed instructions are available at <http://ib.komisc.ru/ExStatR>. The research was partly supported by the Russian Foundation for Basic Research and Government of Komi Republic (18-44-110015).

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The integrated database of geographical distribution of *Darevskia* rock lizard species in the Caucasus and Asia Minor

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Интегрированная база данных географического распределения видов скальных ящериц рода *Darevskia* Кавказа и Малой Азии

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Knowledge of the geographical distribution of parthenogenetic (*D.dahli*, *D.rostombekowi*, *D.armeniaca*, *D.unisexualis*) and their parental bisexual (*D.valentini*, *D.portschinskii*, *D.raddei* (*D.nairensis*), *D. Mixta*) species is important for understanding their biology, for modeling ecological niches and identifying potential range due to accelerating anthropogenic warming and global climate change. Thermoregulation of ectothermic lizards is mainly realized due to the heat received from various thermal factors of the environment. This feature makes them more sensitive to climate change. The new data obtained will allow the broadening of scientific notion of the ecology and speciation of *Darevskia* lizards, and will also help to model possible ways of adaptation of organisms to extreme environmental conditions. The common descriptions of the habitats of *Darevskia* rock lizards are often moved from one publication to another without verification. The purpose of our work is: 1) to create a valid database by developing and carrying out computational experiments with geographic information models by the example of bisexual and parthenogenetic species; 2) to gain new knowledge about the ways and mechanisms of the emergence of hybridization centers for parthenogenetic species and the role of biotic

and abiotic factors in the processes of reticular evolution of vertebrates. The main objectives of the study include the creation of geoinformation models represented by the electronic library of vector maps based on the distribution data of parthenogenetic and their parental species and their contact zones:

1. The model of distribution of 4 parthenogenetic and 4 parental species of rock lizards and the location of possible contact areas in the past, present and in the future;
2. Models of fundamental ecological niches of each species and identification of the main factors influencing the distribution of each species;
3. The model of the evolution of contact zones of parental species and the territory of possible emergence of new forms of rock lizards;
4. The model for predicting changes in the ranges of lizards and their contact areas in the future;
5. The model of the definition of modern zones of possible formation of a new species as a result of stepwise hybridization. The results obtained will allow a correct interpretation of the data of molecular genetics and cytogenetics, and are of essential value for understanding the mechanisms of reticular evolution.

An example of the data analysis for rock lizards of the genus *Darevskia* species shows that standard descriptions of the range of species can include false or ambiguous data. Creating a database of the species presence and documenting the locations is the only way to obtain reliable information on the range of species to understand the mechanisms of the reticular evolution in past, present and future. This study was supported by the RFBR № 18-34-00361, № 17-00-00427.

The use of mathematical methods in analysis of antibioticresistans of microorganisms of lake Baikal

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Long-term studies have shown that in conditions of active anthropogenic pollution of the littoral zone of the Baikal ecosystem, bacterial strains resistant to many antibiotics are observed. Analysis of samples of bacterial resistance to antibiotics studied averaged by the factor of belonging to a certain sampling month and separately by the factor of belonging to a certain year of sampling using the Shapiro-Wilk test showed that the samples under study are not distributed according to the normal law ($P_{value} < \alpha$). In connection with this, the nonparametric Kraskel-Wallis criterion was used for the variance analysis, and for the correlation analysis the nonparametric correlation coefficient of Spearman. The variance analysis of the average resistance of the bacterial community to antibiotics, grouped by the factor of belonging to a certain sampling month, revealed that in different months of the year the average stability significantly differs from each other ($P_{value} = 0.003 < \alpha$).

Analysis of the actual material by season showed that strains of microorganisms resistant to antibiotics can be divided into 2 groups. The first group: antibiotics with relatively small values of the coefficients of variation in the resistance of bacterial communities to them (coefficient of variation < 1). These drugs include: ampicillin, chloramphenicol, neogramone, trimethoprim. The resistance to antibiotics of this group changes to a lesser extent in the transition from season to season. The second group: antibiotics with relatively high values of the coefficients of variation of the resistance of bacterial communities to them ($1 < \text{coefficient of variation} < 1.75$). These are tetracycline, streptomycin, kanamycin, gentamicin, rifampicin, cefazolin, cefatoxime, pefloxacin. The resistance of the bacterial community to the antibiotics of this group is changing to a greater extent, during the five-month period from June to November. It was found that the resistance of bacterial strains to antibiotics varies significantly in different months of the year ($P_{value} = 0.003 < \alpha$).

Dispersion analysis of the average bacterial resistance to antibiotics for the period under review (2005-2006), practically did not reveal the interannual difference in the close years ($P_{value} = 0.34 < \alpha$). When calculating the pairwise correlation coefficients, it was possible to divide antibiotics into three groups. The first - the stability of pairs of antibiotics is formed independently of each other (values of the correlation coefficient $r \approx 0$). The second group consists of pairs with reliable positive values of correlation coefficients ($r > 0$), i.e. the increase in resistance to a single antibiotic was accompanied by an increase in resistance to another antibiotic, the formation of cross-resistance. The third group are pairs of antibiotics with

reliable negative values of correlation coefficients ($r < 0$). In bacterial communities for such pairs of antibiotics, an increase in resistance to a single antibiotic was accompanied by a decrease in resistance to another.

The use of NDVI for the analysis of the effect of drought on forage resources for grazing in the territory of the establishing population of the Przewalski horse *Equus ferus przewalskii* Polj., 1881

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Использование NDVI для анализа влияния засухи на запасы пастбищного корма на территории обитания создаваемой популяции лошади Пржевальского *Equus ferus przewalskii* Polj., 1881

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One of the main challenges for the establishment of semi-free populations of rare hoofed animals in special protected territories is a forecast of forage resources for grazing and their possible changes in years of extreme weather. In 2015, The Russian Government gave a territory for establishing a new protected area called 'Pre-Urals Steppe' to Orenburg State Reserve. A semi-free population of the Przewalski horse *Equus ferus przewalskii* Polj., 1881 has been established in this territory within the

frame of the UNDP/GEF Project ‘Improving the coverage and management efficiency of protected areas in the steppe biome of Russia’. In 2016, vegetation mapping was done and productivity of grassland in the main types of vegetation was analysed by the method of recorded mown plots. A GIS map of vegetation was created and productivity of grassland for grazing was calculated for 2016 which had favourable weather conditions (Fedorov et al., 2018). The aim of the present study is to forecast changes in forage resources for grazing under drought stress. Cloudless Landsat-8 and Sentinel-2 images were used to analyse the normal 2016; cloudless Landsat-5 images were used to analyse the dry 2010. A correlation index of 0.77 between grass productivity in dry weight and NDVI was calculated at the time when the recorded plots were mowed in 2016. A linear regression technique was used to determine the relationship between grass productivity in dry weight and NDVI. The average NDVI at the time when the recorded plots were mowed was calculated for the total grassland area (95% of the protected area); from this information, the forage resources for grazing were determined by the regression equations. The difference between the data obtained by the regression technique and the data from recorded mown plots was 11.4%. The analysis of grasslands for the same period in dry 2010 revealed that the forage resources were almost four times lower than in 2016. Most of vegetation in level and elevated areas dried off in the beginning of July, 2010; they did not recover till the late autumn. It may be predicted that the horses will have difficulties to find forages in winter after a summer drought; a stock of hay must be reserved for such cases.

Use of Remote Sensing data and GIS technologies for monitoring resources of medicinal plants

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**Использование данных ДЗЗ и ГИС-технологий для
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Preservation of the biodiversity of medicinal plants makes it possible to create a basis for the development and creation of new medicines through scientifically based nature management. One of the topical tasks of botanical resource research is the interpretation of plant communities, monitoring their condition and distribution. Remote sensing techniques provide solutions for obtaining, analyzing and managing data at different scales: high-resolution satellite imagery and multi-spectral channels can provide information covering large areas [1], while aerial photography with unmanned aerial vehicles (UAV) allows you to collect comprehensive biometric information from key areas [2]. To carry out quality monitoring of plant communities, the following conditions must be met: regular aerial photography with similar aerial survey parameters to the same phase of vegetation. This will make it possible to obtain the best quality of the original photographic material and successfully interpret the medicinal plants. Studies carried out on the territory of the Tula region in 2014-2017, showed the advisability of using the UAV for monitoring the reserves of wild medicinal plants [2]. The planned accuracy of the created orthophoto, their photographic quality allowed confidently interpret the plant communities during flowering. By stereoscopic images, specialists were able to determine biometric characteristics, such as plant height and number of individuals per square meter, which led to a significant reduction in field work. Plant resources were estimated with an accuracy of not less than 10%. To perform the work, a complex of photogrammetric (PHOTOMOD "Rakurs") and GIS (MapInfo Professional 12). The result of the joint work was a map and database of stocks of medicinal plants for the study site. The use of multispectral aerial and space imagery, in addition to aerial photography data in the visible range, scales the research of medicinal plants resources on significant areas, which should accelerate the work on large areas. Nevertheless, one of the important problems remains the automation of interpretation of wild-growing herb medicinal plants, connected with the peculiarity of the growth of these communities. The solution of the problem is the application of complex analysis using digital terrain models.

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Virtual herbarium collections of the Central Siberian Botanical Garden as a resource for biodiversity study

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Виртуальные гербарные коллекции Центрального сибирского ботанического сада как ресурс для изучения биоразнообразия

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The first herbarium at the Central Siberian botanical garden (CSBG SB RAS) was organized in 1946. Now there are two herbarium collections in CSBG with own acronyms and registration in the Index Herbariorum (NSK and NS). Collection contains about 800 000 herbarium specimens of high vascular plants, mosses, lichens and fungi sampled in Siberia, Russian Far East, Europe, Asia and America. Digitization of high vascular plants was initiated from type specimens by special scanner Herbscan, supported by Andrew Mellon Foundation in 2014. Images and metadata of 800 type specimens are currently available on the Virtual Herbaria web site at the Vienna University, Austria (<http://herbarium.univie.ac.at/database>) and in Jstor (<https://plants.jstor.org>). Special attention was paid to providing on-line high resolution (600dpi) images and metadata for all types specimens (Kovtonyuk, 2015, 2017). In 2017 a new research group “USU-Herbarium” was organized in CSBG SB RAS for digitization and management of herbarium collections, our aim is to provide online access to

CSBG SB RAS herbarium collections as a worldwide resource for biodiversity study. We initiated digitization of NSK and NS high vascular plants collections by two scanners ObjectScan 1600. Currently about 8 000 herbarium specimens were digitized at 600 dpi, images and metadata are stored in CSBG SB RAS Database generated by ScanWizard Botany and MiVapp Botany software (Microtek, Taiwan). The largest number of samples scanned are from Primulaceae (4654), Boraginaceae (632), Athyriaceae (566), Cystopteridaceae (352), Asteraceae (220), Plumbaginaceae (363) and Poaceae (143). The database is structured in a way that a common user can access a specimen file that contains high resolution image and following key information: specimen ID (= barcode), family name, scientific name (genus, species, author of taxon), collector name and collection date, country or administrative region. Alternatively the request may be done by using key words of habitat characteristics, for example, “pine forest”, “meadows”, etc. Images are available for download. In our internal database each image is supplied by the following information: barcode, type status, genus name, species name, author name, subsp /var name, family name, collectors name, field number of herbarium specimen, date (yyyy-mm-dd), country, admin region, latitude degrees, latitude minutes, longitude degrees, longitude minutes, label text, determination name, annotation, Catalogue of Life link and accepted name in CoL. We encourage our fellow colleagues to access herbarium collections online and envision that such a tool will facilitate the progress on worldwide biodiversity studies.

Visualisation model of cereals morphogenesis in the different environments

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Модель визуализации морфогенеза злаков при изменении окружающей среды

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A problem of modelling of processes of growing and development of cereal plants appears in connection with the study of agroecosystem efficiency. Greater amount actual information is collected to this moment. Therefore it is necessary to formalise real data by dynamic models (Stefanova et al., 2006). Until very recently, morphogenesis was difficult to study due to a lack of tools for collecting and handling three-dimensional (3D) information (Kaitaniemi et al., 2000). Our research presents a spatial imitation dynamic model of above-ground morphogenesis in a wheat (*Triticum aestivum* L.). Functions and parameters describing structural development were obtained from three-dimensional (3D) measurements of plants made at intervals during their development. Seven cultivars and 9 variations of environment were used. The algorithms were expressed as specifications of morphogenesis in specific sistem formalism like as L-sistem formalism (Allen et al., 2005) and the specifications were interpreted by specialized software to create 2D wheat plants. Using the length of metamer organs, realistic images were generated of the lengths and shapes of subsequent leaves. The approach captures the dynamic interaction between partitioning and morphogenesis and presents the complex results as images that aid rapid interpretation (Sheloukhova, Stefanova, 2015). The model used specific system productions to capture developmental events, such as the initiation of new metamers. The visualization program was written on programming language C++. Using the length of metamer organs, it generates realistic images of the lengths and shapes of subsequent leaves. On output it exacts average plant ontogeny scheme. Program has its interface, which does its available for many users. Data are carried in the type of pattern or tables. Particularity of program is a demonstration of changing the particularities of plant morphogenesis of different cultivars depending on conditions of ambience at different vegetation periods. Side-view comparison of real wheat plants, growing in the different environments was done. Program is designed for conduct of both and new cereals genotypes and ecological different environments.

Web-GIS “Faunistics” – the online database for crowdsourcing data collecting on biodiversity

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Веб-ГИС «Фаунистика» для краудсорсингового сбора информации о биоразнообразии

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Web-GIS "Faunistics" was launched on the Internet on December 12, 2012, at wildlifemonitoring.ru the developers of the program are I.V. Karyakin, D.A. Kamenskiy, and E.A. Grachev. "Faunistics" is supported by Sibecocenter LLC and Panoptica LLC (Novosibirsk). The source is used by governmental authorities for maintaining databases on Red Lists of Endangered Species for Samara and Altai Regions of Russia. "Faunistics" is implemented on the basis of server software under Linux operating system Ubuntu 11.10, web server Apache 2.2.20, MySQL 5.7 database, PHP 5.4 interpreter and Python 2.7 and is developed on the basis of the GoogleMaps API. The client part is written in jQuery and Knockout. The cartographic basis used in the web-based GIS "Faunistics" consists of vector topographic maps from GoogleMaps, OpenStreetMap, Yandex-maps, and ArcGIS, as well as satellite imagery coverage from GoogleMaps and Bing. "Faunistics" is a crowdsourcing system for the data collecting from the wide range of users who have access to the Internet as well as geo-referencing photo-hostings. Users can add, store and export data and geo-layers consist of polygonal, linear and point objects. Data export is possible in HTML (photo-report), CSV, KML/KMZ, GPX, SHP, and MapInfo files, and in MSWord DOC-files (report). Web-interface of "Faunistics" is written in Russian and English. From August 22, 2014 we implement the loading of protected area layers from the web-GIS "Protected Areas of Russia" to "Faunistics"; on October 5, 2015 the import of observations from the database "Online Diary of bird observations"; from September 1, 2016 "Faunistics" stored a data from the bioresource collection of the N.K.Koltsov Institute of Developmental Biology RAS; and since December 15, 2016, it has been integrated into GBIF. The most dynamically developed part of the "Faunistics" is "Raptors of the world" section – it contains 76 880 photos in 44 324 observations by 152 users.

A “Nestboxing” section contains 2 113 photos in 1 603 observations by 13 users. A “Birds of Northern Eurasia” section is a section of the Novosibirsk community of birdwatchers and it contains 13 571 photos in 43 198 observations by 74 users. A section “Small cats of Eurasia” is a section maintained by the working group on study and conservation of Pallas Cat in Eurasian Steppes, and it contains 886 photos in 570 observations by 37 users. A section “Semiaquatic mammals of Eurasia” is a section of initiative group on the conservation of Russian desman and it represents the most completed source of information on observations of living colonies of the species from 1949 to 2015. It contains 38 photos in 1 254 observations by 3 users. A section “Protected areas and anthropogenic disturbances” contains 1 265 photos in 541 observations by 14 users. This section is in big practical use – it allows users for rapid completing and printing acts for appeals to the prosecutor’s office on violations of environmental legislation.

Wild forest reindeer habitat assessment in forest landscapes of eastern part of Barentz region

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Boreal forests provide significant ecosystem services i.e. biodiversity and other non-timber resources. Habitat loss is globally a threat to biodiversity and in managed boreal forests a loss of habitats is the most common factor affecting species diversity. We made an attempt to implement classification of habitats and their ecological assessment regimes of the pristine forests landscape of Barents region. The forested watershed are richly inhabited by endangered plant, fungi and vertebrate species, many of which are red listed. They exhibits high diversity of natural ecosystems and can be viewed as a representative example of the European middle and northern taiga with preserved gradient of different successional stages and habitat types. The watershed forests are home to one of the last and the most southern remaining populations of listed wild forest reindeer

(*Rangifer tarandus*). To prepare maps for wildlife habitat assessment we mapped vegetation cover, disturbances, sandy soils and roads. Classification of vegetation cover was carried out on the base of remote sensing, forestry maps and big series of field data. To assign the classes for the selected Landsat 8 pixels, we used the following data. GPS ground data series were available for different years. This information was used jointly with high-resolution images Sentinel 2. To classify the Landsat 8 images the random forest algorithm (RF in NextGis) was used on the base of training points (Belgiu Drogut 2016). The random generation was repeated 10 times. To generalize the vegetation map LSL tool was used (Rempel et al. 2015). Modern conservation planning often uses a particular type of habitat model called a resource selection function (RSF) or a resource selection probability function (RSPF). These functions can estimate the probability that a particular piece of land will be selected for use by the species of interest. Low probabilities of use associated with deciduous forests and areas with high linear feature density are consistent with predation risk avoidance and landscapes with high amounts of deciduous cover and high density of low traffic linear features. Reindeer selection for old growth conifer cover is also consistent with predation risk avoidance as well as browse availability. The models can be used to estimate changes in expected patterns of use based on forecast changes to the landscape.